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Applicant: WANG, et al

Title: **PRIMERS, METHODS AND KITS FOR AMPLIFYING OR
DETECTING HUMAN LEUKOCYTE ANTIGEN ALLELES**

Appl. No.: Unknown

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**PROVISIONAL PATENT APPLICATION
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Sir:

Transmitted herewith for filing under 37 C.F.R. § 1.53(c) is the provisional patent application of:

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Enclosed are:

[X] Specification, Claims and Abstract (including figures) (106 pages).

The filing fee is calculated below:

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PATENT APPLICATION

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicants: Lu Wang *et al.*

Title: **PRIMERS, METHODS AND KITS FOR AMPLIFYING OR DETECTING
HUMAN LEUKOCYTE ANTIGEN ALLELES**

Atty. Docket No.: 028979-0151

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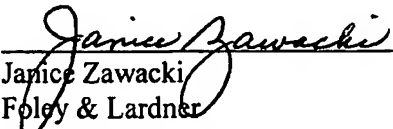
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U.S. PROVISIONAL PATENT APPLICATION

for

**PRIMERS, METHODS AND KITS FOR AMPLIFYING OR DETECTING HUMAN
LEUKOCYTE ANTIGEN ALLELES**

1

PRIMERS, METHODS AND KITS FOR AMPLIFYING OR DETECTING HUMAN LEUKOCYTE ANTIGEN ALLELES

SUMMARY OF THE INVENTION

[0001] Embodiments of the present invention are set forth below:

[0002] A primer set comprising:

primers that are capable of amplifying all human leukocyte antigen (HLA) alleles of an HLA locus; and

a control primer pair that will produce an HLA control amplicon of predetermined size from the one or more HLA alleles if the one or more HLA alleles are present in the sample.

[0003] The primer set of the previous paragraph wherein the portion of the HLA allele amplified by the control primer pair is common to all or substantially all HLA alleles.

[0004] The primer set of paragraph [0002] or [0003] wherein the portion of the HLA allele amplified by the control primer pair comprises a portion of exon 4 of the HLA A locus or HLA B locus.

[0005] The primer set of any one of paragraphs [0002] to [0004] wherein the HLA control amplicon is about 500, 600, 700, 800, 900 or 1000 base pairs in length.

[0006] The primer set of any one of paragraphs [0002] to [0005] wherein the one or more HLA alleles are common to a single HLA locus.

[0007] A method for amplifying an HLA allele comprising:
performing a nucleic acid amplification reaction on a sample having or suspected of having one or more HLA alleles wherein the nucleic acid amplification reaction

comprises a primer set that is capable of amplifying one or more HLA alleles and a control primer pair that will produce an HLA control amplicon of predetermined size from the one or more HLA alleles if the one or more HLA alleles are present in the sample thereby providing an indication the presence of absence of HLA allele amplification.

[0008] The method of the previous paragraph wherein the portion of the HLA allele amplified by the control primer pair is common to all or substantially all HLA alleles.

[0009] The method of paragraphs [0007] or [0008] wherein the portion of the HLA allele amplified by the control primer pair comprises a portion of exon 4 of the HLA A locus or HLA B locus.

[0010] The method of any one of paragraphs [0007] to [0009] wherein the HLA control amplicon is about 500, 600, 700, 800, 900 or 1000 base pairs in length.

[0011] The method of any one of paragraphs [0007] to [00010] wherein the one or more HLA alleles are common to a single HLA locus.

[0012] A primer set comprising:
a mixture comprising a plurality of primers that are capable of simultaneously amplifying a plurality of a portion of class I HLA alleles simultaneously.

[0013] The primer set of the previous paragraph wherein the plurality of Class I HLA alleles belong to the same HLA locus.

[0014] The primer set of the previous paragraph wherein the HLA locus is HLA A or HLA B.

[0015] The primer set of the previous paragraph wherein the plurality of primers are capable of producing two amplicons spanning all alleles from the HLA locus.

[0016] The primer set of the previous paragraph wherein the first amplicon spans exon 1 to intron 3 and the second amplicon spans intron 3 to exon 5.

[0017] A method for amplifying a class I HLA allele comprising:
performing a nucleic acid amplification reaction on a sample having or suspected of having a class I HLA allele wherein the nucleic acid amplification reaction comprises the primer set of any one of paragraphs [0012] to [0016].

[0018] The method of any one of paragraphs [0007] to [00011] or [0017]:
sequencing any resulting HLA amplicons.

[0019] A primer for sequencing an HLA allele comprising:
a forward primer comprising a 3' portion and a 5' portion wherein the 3' portion is complementary to an HLA allele of interest and the 5' portion is not complementary to the HLA allele of interest.

[0020] The primer of the previous paragraph wherein the 5' portion non-complementary portion is 1 to about 35 bases inclusive.

[0021] The primer of paragraphs [00019] or [0020] wherein the forward primer is for one of exons 2 and 3 in a B locus of the HLA allele.

[0022] The primer of any one of paragraphs [0019] to [0021] 18-20 further comprising one or more additional primers that are complementary to one or more additional HLA alleles of interest.

[0023] A method for determining the sequence of an HLA allele comprising:

performing a sequencing reaction on an HLA allele using the primer of any one of paragraphs [0019] to [0022] 18-21; and
determining the sequence of one of more HLA alleles.

BRIEF DESCRIPTION OF THE DRAWINGS

[0024] Figure 1 is a flowchart illustrating a specific procedure for sequencing an HLA allele according to a present method.

[0025] Figures 2A-2D are sequencing Electropherograms from the example.

DETAILED DESCRIPTION

[0026] Described herein are primer sets, methods and kits for amplifying and/or detecting human leukocyte antigen alleles. Some embodiments of the present invention provide primer sets and methods for amplifying HLA alleles.

[0027] On such primer set includes primers that are capable of amplifying all HLA alleles of an HLA allele subset or locus and also a control primer pair that is capable of producing an HLA amplicon of a defined size if the one or more HLA alleles are present in the sample. This primer set utilizes the target HLA allele as the template for the control primer pair and provides an indication the presence of absence of one or more HLA alleles. Any HLA alleles of the HLA allele subset or locus are also the template for the other primers in the primer set. As will be understood by the skilled artisan, in order to provide an effective control, the portion of the HLA allele amplified by the control primer pair is typically common to all or substantially all HLA alleles being tested for. In some embodiments, particularly when the target HLA locus is HLA A or HLA B, the portion of the HLA allele amplified by the control primer pair comprises a portion of exon 4. The primer set can be used in an amplification reaction to amplify an HLA allele and also provide a control. The control primer pair provides an indication of the efficiency of

any HLA allele amplification that occurs in the amplification reaction and also prevents false negative results. For example, if the results of the amplification provide an amplicon but lack the control amplicon, then the amplicon is likely a false negative. In contrast, if the control amplicon is also present then the amplification produced a positive result. In some embodiments, the primers of the control primer pair are selected such that any amplicon they produce will have a substantially constant size, such as 500, 600, 700, 800, 900 or 1000 base pairs, regardless of the HLA alleles that are present in the sample. As long as they do not interfere with the control parameters, the control primer pair can span a region with or without polymorphic positions. Accordingly, the portion of the HLA allele amplified by the control primer pair can have base polymorphisms but should lack any significant insertions or deletions.

[0028] Another primer set of the present invention contains a plurality of primer pairs, typically in the same solution, that are capable of simultaneously amplifying a plurality of class I HLA alleles simultaneously. As such, this primer set is capable of performing a successful multiplex amplification for all HLA alleles of an HLA allele subset or locus, such as the A locus, B locus or DR loci. In some embodiments, this multiplex amplification is achieved while still maintaining locus specificity because the product sizes produced from the amplification are considerably smaller.

[0029] Primer sets having combinations of the above characteristics can also be used. The above primer sets can be used to amplify any HLA alleles that are present in a sample.

[0030] The above primers and primer sets can be used in reaction that amplify HLA alleles. Suitable amplification reactions include those that proceed both linearly and exponentially. The present methods are also simplified as they can provide a common sequencing protocol for all HLA loci. Generally, the above

primer sets will contain primers that are sufficient to amplify all alleles of an HLA locus, such as HLA A, HLA B, etc. in a single reaction. Accordingly, the primers can be targeted to hybridize to non-specific regions of the chosen HLA locus so that all different HLA alleles can be successfully amplified. The primers can also be located so that the HLA amplicon resulting from the primers spans enough polymorphic positions of the locus so that individual alleles can be identified in a subsequent sequencing or typing reaction utilizing the HLA amplicon.

[0031] In some embodiments, where HLA A locus alleles are being amplified, the present primers can be selected to provide a single amplicon that includes exons 2, 3 and 4. Where HLA B locus alleles are being amplified, different primer sets can be used to produce dual amplicons that cover exons 2, 3 and 4. Some embodiments of the present primer sets, methods and kits utilize two separate amplifications in the B locus that reduces the number of potential heterozygotic combinations resulting in simplified sequence analysis, and the position of these split primers results in resolution of more of the locus thus reducing further the number of resultant ambiguities. For example, this can be achieved by amplifying the regions from exon 1 to intron 3 and intron 3 to exon 5 as two separate products simultaneously in one amplification mix. This results in a much more robust amplification. Amplifying these regions as two separate products is advantageous over a single product as this single product is frequently weak and hard to see on an agarose gel, particularly when modified nucleotides are required.

[0032] General and non-limiting position strategies for these primers is set forth in Table 1. In fact, the primer hybridization positions shown in this table can often be varied by one, two, five, ten, twenty or more positions, either upstream or downstream, and still provide acceptable results. Typically, when the primer hybridization position is moved upstream of the position illustrated in the table then additional bases can be added to the primer that hybridize further upstream which

can be accompanied by removal of bases from the opposite end of the primer. Similarly, when the hybridization position is moved downstream then bases are added to the primer that hybridize further downstream which can be accompanied by the removal of bases on the upstream hybridizing portion of the primer.

In HLA DR locus (Class II) amplification, one embodiment provides for a primer set that allows for eleven group specific amplifications that achieve resolution of DRB1, DRB3, 4 and 5 and exon 2.

[0033] The primers of the primer sets 3' terminus are capable of being extended by a nucleic acid polymerase under appropriate conditions and can be of any length, for example ranging from about 5 nucleotides to several hundred. Preferably, the primer oligonucleotide will have a length of greater than 10 nucleotides, and more preferably, a length of from about 12-50 nucleotides, such as 12-25 or 15-20. The primer oligonucleotides can also be chosen to have a desired melting temperature, such as about 40 to about 80°C, about 50 to about 70°C, about 55 to about 65°C, or about 60°C. The length of the primer is sufficient to permit the primer oligonucleotide to be capable of hybridizing to the target molecule. The sequence of the primer oligonucleotide is selected such that it is complementary to a predetermined sequence of the target molecule.

[0034] The present primer pairs can also be used individually to identify a single HLA allele, as desired. The present primers can be used in any method where nucleic acid primers find utility. For example, the primers are readily applicable to RT PCR of HLA mRNA for expression analysis because they target exon regions. The present primers can also be extended to, as yet, unknown HLA alleles.

[0035] One example of an assay where the present primer pairs find use include a detection assay or method for identifying an HLA allele in a sample

having, or suspected of having an HLA allele. In such an assay, generally, the sample will be contacted with the primer set under conditions such that the primer pair will amplify the HLA locus for which the primer pair is specific, if that locus is present in the sample. The presence or absence of the amplicon can then be determined or detected by standard techniques, such as separation techniques including electrophoresis, chromatography (including HPLC and denaturing-HPLC), or the like. Exemplary techniques for performing these assays are described in the examples section. As will be recognized by the skilled artisan the production of an amplicon will indicate the presence of an HLA locus in a sample. Accordingly, the presence or absence of an amplicon can be correlated with the presence or absence of the HLA locus in the sample. The sample to be detected can be obtained from any suitable source or technique.

[0036] Typically, nucleic acid amplification or extension involves mixing a target nucleic acid with a "master mix" containing the reaction components for performing the amplification reaction and subjecting this reaction mixture to temperature conditions that allow for the amplification of the target nucleic acid. The reaction components in the master mix can include a buffer which regulates the pH of the reaction mixture, one or more of the four deoxynucleotides (dATP, dCTP, dGTP, dTTP - preferably present in equal concentrations), that provide the energy and nucleosides necessary for the synthesis of DNA, primers or primer pairs that bind to the DNA template in order to facilitate the initiation of DNA synthesis and a DNA polymerase that adds the deoxynucleotides to the complementary DNA strand being synthesized. The polymerase used in the present methods and kits is not particularly limited, and any suitable polymerase can be used. Examples of suitable polymerase include thermostable polymerase enzymes, such as the TAQ polymerase. Preferred polymerases have low error rates.

[0037] A typical thermal cycling reaction used in DNA amplification has a temperature profile of thermal cycling that involves an initial ramp up to a predetermined, target denaturation temperature high enough to separate the double-stranded target DNA into single strands. Generally, the target denaturation temperature of the thermal cycling reaction is approximately 91-97°C, such as 94°C- 96°C, and the reaction is held at this temperature for a time period ranging between 20 seconds to two minutes. Then, the temperature of the reaction mixture is lowered to a target annealing temperature which allows the primers to anneal or hybridize to the single strands of DNA. Annealing temperatures can vary greatly depending upon the primers and target DNA used. Generally, annealing temperatures range from 58°C - 70°C depending upon the application. Next, the temperature of the reaction mixture is raised to a target extension temperature to promote the synthesis of extension products. The extension temperature is generally held for approximately two minutes and occurs at a temperature range between the annealing and denaturing temperatures. This completes one cycle of the thermal cycling reaction. The next cycle then starts by raising the temperature of the reaction mixture to the denaturation temperature. Typically, the cycle is repeated 25 to 35 times to provide the desired quantity of DNA. As will be understood by the skilled artisan, the above description of the thermal cycling reaction is provided for illustration only, and accordingly, the temperatures, times and cycle number can vary depending upon the nature of the thermal cycling reaction and application.

[0038] Accordingly, the present primers, methods and kits can be used for research and clinical applications for any HLA associated disease, disorder, condition or phenomenon.

[0039] The present amplifications are preferably performed with a reaction volume and amount that is sufficient to perform a separation or detection step in

addition to providing enough amplified product in order to perform a sequencing reaction. Typically, amplification reactions having 25 μ l or more total volume are sufficient.

[0040] In some embodiments, a single multiplex amplification reaction can be run for all major HLA loci, e.g. HLA A, HLA B, HLA C, etc. in a single vessel. Generally, separate amplification reactions will be run for each HLA loci separately, and any of these separate reactions can employ a non-multiplex approach that produces amplicons that encompass all of the desired locus or a multiplex approach to produce amplicons that encompass shorter segments of the amplified locus. Such reactions can be run simultaneously or subsequently as desired.

[0041] Some of the present embodiments also provide complete locus resolution by employing locus specific primers located in the 5' and 3' untranslated areas of the gene. This can be approached in two distinct ways. The first can utilize an expansion and enhancement of the multiplex approach, where the entirety of the locus would be amplified from genomic DNA resulting in two or more products created simultaneously. This could be accomplished by two larger products, or potentially three smaller products. Secondly, amplification of the locus using RNA as the starting template through simultaneous RT/PCR could provide total locus coverage with a manageable single product. This would provide ultimate resolution of HLA types.

[0042] After the HLA locus is amplified the specific alleles of the locus can then be determined by any method or assay known in the art. One such method is a sequencing reaction, for example the Sanger sequencing method. A description of such a general and specific sequencing method is set forth in Figures 1 and 1A. A detailed methodology is set forth in Appendix II. This sequencing reaction can be facilitated using a DYEnamic™ ET* Terminator Cycle Sequencing Kits available from Amersham Biosciences. Other suitable sequencing protocols include sequencing by

synthesis protocols, such as those described in U.S. Patent Nos. 4,863,849, 5,405,746, 6,210,891, and 6,258,568 and PCT applications WO 98/13523, WO 98/28440, WO 00/43540, WO 01/42496, WO 02/20836 and WO 02/20837.

[0043] Also provided is a primer set for sequencing HLA alleles and methods of sequencing HLA alleles which can use these primer sets. In some of these sequencing primers or detection methods, the 5' portion of one or more of the sequencing primers contains nonhomologous or sequence that does not hybridize to the HLA allele that can provide enhanced resolution of the sequence generated early in the polymerization reaction. Typically, the first bases resolved on any sequencing system are unclear. This tends to improve within 30 to 35 bases from the 5' end of the sequencing primer. By having or adding additional bases to the 5' end of the sequencing primer, the present primers with the non-complementary portion can achieve enhanced resolution of sequence. This design is particularly useful in sequencing primers that hybridize close to, for example within 10, 15, 20, 25, 30 or bases, of an intron/exon junction, for example where locus structure dictates placement of the primer close to the junction, such as occurs in exons 2 and 3. The number of the additional nonhybridizing bases on the 5' end of the specified sequencing primers can vary as desired, and for example can be one to 35 bases, such as two, three, four five, ten, fifteen, twenty, etc.

[0044] In some embodiments, HLA allele amplification can be joined together with an HLA sequencing reaction. Accordingly, the present primer sets, methods and kits can resolve greater than or about 50%, 55%, 60%, 65%, 70%, 75%, 80% or more of cis/trans ambiguities, including those found in the HLA B locus.

10X PCR Buffer

Tested from 0.5X- 2X concentration in the reaction, such as 1X.

MgCl₂

Class I reaction can typically range from 1.0mM – 2.0mM concentration in the reaction, for example 1.5mM.

Class II reaction from 1.5mM – 2.5mM concentration in the reaction, e.g., 2.0mM for one tube and 2.5mM for group specific amplification.

dNTP

0.5% - 2% concentration in the reaction, such as 1%.

[0045] For Class I, DMSO can be used at 5%-15% concentration in the reaction, for example 8%.

[0046] Primer concentration can vary and was successfully at ranges of 10 pmol/μl – 30 pmol/μl although optimal concentrations vary depending upon the reaction conditions, primer sequence and target sequence.

Product Specifications/QC Criteria

Background: Less than 20% of overall signal.

Evenness of the peaks: Must not be more than 30% difference. (I'm trying to get this changed to 50% difference)

Average signal strength:

Capillary = 100units – 4000 units. This is a very large range. But it was left that way to cover our bases. Typically, when signals get above 2000-2500 units, excessive background will result.

377 = 40 units – 4000units.. There is really no upper limit on this because the signals never get above about 500 units on the 377.

Coverage: The full sequence of the exon in question is readable from beginning to end.

[0047] Accordingly, preferred methods focus on identifying HLA alleles. The alleles of the HLA loci are classified as Class I – HLA-A, HLA-B, HLA-C, HLA-E, HLA-F and HLA-G, or Class II - HLA-DRA, HLA-DRB1, HLA-DRB2-9, HLA-DQA1, HLA-DQB1, HLA-DPA1, HLA-DPB1, HLA-DMA, HLA-DMB, HLA-DOA and HLA-DOB. There are over a hundred identified alleles that fall in some of these loci and these alleles are closely related and can differ in sequence by only one, or a few, positions. The HLA gene is discussed by Schreuder et al. in Tissue Antigens, 58:109 (2001) and the references disclosed therein, all of which are incorporated by reference. Additional information regarding HLA alleles, and in particular sequence information is available at www.ebi.ac.uk/imgt/hla and www.anthonynolan.org.uk/research.html.

[0048] Any or all of the present primers can be labeled with a detectable moiety, if desired, to facilitate detection. When present, the detectable moiety of the present invention is not particularly limited. Suitable examples of detectable labels include fluorescent molecules, beads, polymeric beads, fluorescent polymeric beads and molecular weight markers. Polymeric beads can be made of any suitable polymer including latex or polystyrene.

[0049] The present invention also provides arrays of the present primers that are contained within distinct, defined locations on a support. In some embodiments, the primers will be attached to the support in the defined location. The primers can also be contained within a well of the support. Each defined, distinct area of the array will typically have a plurality of the same primers. As used herein the term well is used solely for convenience and is not intended to be limiting. For example, a well can include any structure that serves to hold the nucleic acid primers in the defined, distinct area on the solid support. Non-limiting

example of wells include depressions, grooves, walled surroundings and the like. In some of the arrays, the primers at different location can have the same probing regions or consist of the same molecule. This embodiment is useful when testing whether nucleic acids from variety of sources contain the same target sequences. The arrays can also have primers with one or different primer regions at different location within the array. This embodiment can be useful where nucleic acids from a single source are assayed for a variety of target sequences. Combinations of these array configurations are also provided where some of the primers in the defined locations contain the same primer regions whereas other locations contain primers with primer regions that are specific for different targets. Any suitable support can be used for the present arrays, such as glass or plastic, either of which can be treated or untreated to help bind, or prevent adhesion of, the primer. In some embodiments, the support will be a multi-well plate so that the primers need not be bound to the support and can be free in solution. Such arrays can be used for automated or high volume assays for target nucleic acid sequences.

[0050] Although the present primers generally utilize the five standard nucleotides (A, C, G, T and U) in the nucleotide sequences, the identity of the nucleotides or nucleic acids used in the present invention are not so limited. Non-standard nucleotides and nucleotide analogs, such as peptide nucleic acids and locked nucleic acids can be used in the present invention, as desired. Several nucleotide analogs are known in the art (e.g., see, in Rawls, C & E News Jun. 2, 1997 page 35; in Brown, Molecular Biology LabFax, BIOS Scientific Publishers Limited; Information Press Ltd, Oxford, UK, 1991). In addition, the bases in a sequence may be joined by a linkage other than a phosphodiester bond, so long as the bond does not interfere with hybridization, such as in a peptide nucleic acid. These nucleotide analogs include any of the known base analogs of DNA and RNA such as, but not limited to, 4-acetylcytosine, 8-hydroxy-N6-methyladenosine, aziridinylicytosine, pseudoisocytosine, 5-(carboxyhydroxymethyl) uracil, 5-

fluorouracil, 5-bromouracil, 5-carboxymethylaminomethyl-2-thiou- racil, 5-carboxymethylaminomethyluracil, dihydrouracil, hypoxanthine, inosine, N6-isopentenyladenine, 1-methyladenine, 1-methylpseudouracil, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-methyladenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxy-aminomethyl-2-thiou- racil, beta-D-mannosylqueosine, 5'-methoxycarbonylmethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid, oxybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, N-uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid, pseudouracil, queosine, 2-thiocytosine, orotic acid, 2,6-diaminopurine and the AEGIS™ bases isoC and isoG. As such, the primers can contain DNA, RNA, analogs thereof or mixtures (chimeras) of these components.

[0051] Universal nucleotides can also be used in the present primers. As used herein, universal nucleotide, base, nucleoside or the like, refers to a molecule that can bind to two or more, i.e., 3, 4, or all 5, naturally occurring bases in a relatively indiscriminate or non-preferential manner. In some embodiment, the universal base can bind to all of the naturally occurring bases in this manner, such as 2'-deoxyinosine (inosine). For example, the universal base can bind all of the naturally occurring bases with equal affinity, such as 3-nitropyrrole 2'-deoxynucleoside (3-nitropyrrole) and those disclosed in U.S. Patent Nos. 5,438,131 and 5,681,947. Generally, when the base is "universal" for only a subset of the natural bases, that subset will generally either be purines (adenine or guanine) or pyrimidines (cytosine, thymine or uracil). Examples of nucleotides that can be considered universal for purines are known as the "K" base (N6-methoxy-2,6-diaminopurine), as discussed in Bergstrom et al., *Nucleic Acids Res.* 25:1935 (1997) and pyrimidines are known as the "P" base (6H,8H-3,4-dihydropyrimido[4,5-c][1,2]oxazin-7-one), as discussed in Bergstrom et al., *supra*,

and U.S. Patent No. 6,313,286. Other suitable universal nucleotides include 5-nitroindole (5-nitroindole 2'-deoxynucleoside), 4-nitroindole (4-nitroindole 2'-deoxynucleoside), 6-nitroindole (6-nitroindole 2'-deoxynucleoside) or 2'-deoxynebularine. A partial order of duplex stability has been found as follows: 5-nitroindole > 4-nitroindole > 6-nitroindole > 3-nitropyrrole. When used, such universal bases can be placed in polymorphic positions, for example those that are not required to specifically identify an allele. Combinations of these universal bases can also be used as desired. Primers and strategies using universal primers are discussed in U.S. Patent Application Serial No. 10/429,912.

[0052] The present invention also provides kits for carrying out the methods described herein. In one embodiment, the kit is made up of one or more of the described primer pairs with instructions for carrying out any of the methods described herein. The instructions can be provided in any intelligible form through a tangible medium, such as printed on paper, computer readable media, or the like. A plurality of each primer pair can be provided in a separate container for easy aliquoting. The present kits can also include one or more reagents, buffers, hybridization media, salts, nucleic acids, controls, nucleotides, labels, molecular weight markers, enzymes, solid supports, dyes, chromatography reagents and equipment and/or disposable lab equipment, such as multi-well plates (including 96 and 384 well plates), in order to readily facilitate implementation of the present methods. Such additional components can be packaged together or separately as desired. Solid supports can include beads and the like whereas molecular weight markers can include conjugatable markers, for example biotin and streptavidin or the like. Enzymes that can be included in the present kits include DNA polymerases and the like. Examples of preferred kit components can be found in the description above and in the following examples.

[0053] One embodiment of kit according to the present invention that can amplify and sequence HLA alleles is described below:

A Locus

Amplification Primers:

The 5' primer begins in the A Locus 5' untranslated region and ends in exon 1. The 3' primer is in exon 5. This is a locus specific amplification and all alleles are amplified with this primer set.

Sequencing Primers:

All sequencing primers are located in the introns flanking exons 2, 3 and 4.

B Locus

Amplification Primers:

Two 5' primers in exon 1. The alleles are divided roughly in half between the two primers as follows:

C Group		G Group		
070201	380201	1301	4002	5611
070202	390101	1302	4003	570101
0703	390103	1303	4004	5702
0704	390201	1304	4005	570301
0706	390202	1308	400601	5706
0709	3903	180101	400602	5801
0718	3904	1802	4008	5802
0801	3905	1803	4013	5804
0802	390601	1806	4020	5901
1401	390602	2702	44020101	7801
1402	3908	2703	44020102S	780201

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1405	3909	2704	440301	8101
15010101	3910	270502	440302	8202
1502	3917	270504	4404	8301
1503	3924	270505	4406	
1508	400101	2706	4407	
1509	400102	2708	4408	
1510	4007	2709	4409	
151101	4012	2711	4413	
151102	4016	2712	4431	
1512	4023	2713	47010101	
1513	4101	2714	47010102	
1514	4102	2718	4702	
1515	4201	350101	510101	
1516	4418	3502	510102	
151701	4501	3503	510105	
151702	4504	3504	510201	
1518	4601	3505	510202	
1519	4801	3506	5103	
1520	4802	3507	5104	
1521	4805	3508	5108	
1523	4901	3511	520101	
1525	5001	3512	520102	
1528	5002	3515	5204	
1529	670101	3528	5301	
1546	6702	3531	5401	
1552	7301	3541	5501	
1553		3542	5502	
1554		3543	5505	

1555	3701	5512
1557	3702	5601
1558	3704	5602
1566	3705	5603

There are four 3' primers in exon 5 (primers are multiplexed to cover the complexity of B Locus in this exon.)

Sequencing Primers:

All sequencing primers are located in the introns flanking exons 2, 3 and 4.

DRB1 One Tube

Amplification Primers:

[0054] There are 6 5' amplification primers which begin in intron 1 and end in exon 2. The primers are each designed to amplify a specific group of alleles: DRB1*01, DRB1*15/16/07, DRB1*03/11/13/14/8/12, DRB1*04, DRB1*09, and DRB1*10.

[0055] There is one 3' primer located in exon 2. All amplification primers are tailed with the M13 sequence. M13 sequence are tails added to the amplification primers, such as in DR and DQ, that allow the utilization of a single forward and reverse primer irrespective of groups. This results in a reduction in the total number of sequencing primers that must be included in the kit to cover all possible products. The tailing of the amplification primers was also done to assure full coverage of exon 2 upon sequencing.

Sequencing primers:

The sequencing primers are M13 forward and M13 reverse.

DRB1/3/4/5 Group Specific

Amplification primers:

[0056] The primers either begin in intron 1 and end in exon 2 or are fully in exon 2 depending on where the most specificity is for the group of alleles being

amplified. There are 11 5' Group specific primers amplifying the following groups/beta chains:

DRB1*01, DRB1*15/16, DRB1*03/11/13/14, DRB1*04, DRB1*07, DRB1*8/12, DRB1*09, DRB1*10, DRB3, DRB4, DRB5.

There is one 3' primer located in exon 2.

[0057] All amplification primers are tailed with the M13 sequence. The tailing of the amplification primers was done to assure full coverage of exon 2 upon sequencing.

[0058] Sequencing primers: The sequencing primers are M13 forward and M13 reverse.

[0059] Exemplary, but non-limiting, primer sets are described in the Tables and Appendices. Sequence alignments for assigning positions can be obtained by comparing the listed sequences with reported HLA sequences which can be found at www.ebi.ac.uk/imgt/hla and www.anthonynolan.org.uk/research.html. In the reported sequences, letter other than A, C, G or T indicate non-standard universal bases as follows: R, Y, S, M, W, and K are degenerate bases consisting of two possible bases at the same position. A or G = R, C or T = Y, G or C = S, C or A = M, A or T = W and G or T = K. There are also combinations of 3 possible bases at a particular base position known as H, B, V. Although primer pairs are often used in nucleic acid amplifications, the present primer sets can contain odd numbers of primers so that one or more forward primers can work in conjunction with a single reverse primer to produce an amplicon and vice versa. Appendix I provides a list of exon identities and ambiguous typing combinations of some HLA alleles that can be resolved by the present primer sets, methods and kits. Preferred kits include all reagents, primers, equipment etc. needed to perform the HLA amplification and/or sequencing except for the sample to be tested.

EXAMPLES

[0060] A and B Locus Multiplex Amplification

Genomic DNA was amplified with the following amplification mix:

A Locus

Reagent	Amount
Purified water	9.3ul
10X PCR Buffer	2.5ul
Magnesium Chloride	1.5ul
DMSO	2.0ul
dNTP (50% deazaG)	2.5ul
5'Primer- pA5-5	0.5ul
3'Primer- pA3-31	0.5ul
5'Primer- pA5-3	0.5ul
3'Primer- pA3-29-2	0.5ul
FastStart Taq	0.2ul
Genomic DNA	5.0ul
25ul total reaction volume	

B Locus

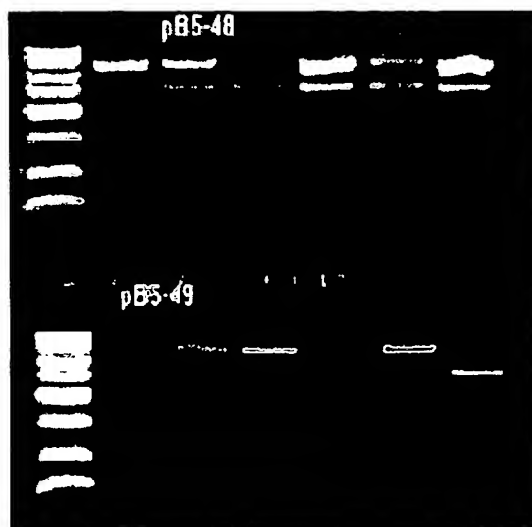
Reagent	Amount
Purified water	9.3ul
10X PCR Buffer	2.5ul
Magnesium Chloride	1.5ul
DMSO	2.0ul
dNTP (50% deazaG)	2.5ul
5'Primer- pB5-48 or 5-49	0.5ul
3'Primer- pB3-24	0.5ul
5'Primer- pB5-55 + 4	0.5ul
3'Primer- pA3-20,21,22,23	0.5ul
FastStart Taq	0.2ul
Genomic DNA	5.0ul
25ul total reaction volume	

The samples were run in a PE 9700 thermal cycler under the following conditions:

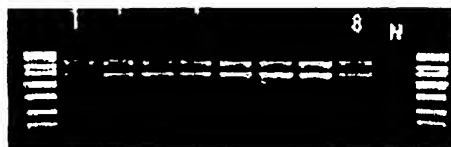
Initial Denaturation	95°C	4 min	
Denaturation	95°C	20 sec	
Annealing	63°C	20 sec	35 cycles
Extension	72°C	40 sec	
Final Extension	72°C	5 min	

The PCR amplicons were run on a 1.5% agarose gel

B Locus Agarose gel



A Locus Agarose gel



For A Locus, the 1200bp band is the product from pA5-3 and pA3-31 and the smaller 700bp band is the product from pA5-5 and pA3-29-2.

For B Locus, the 1200bp band is the product from pB5-48 or pB5-49 and pB3-24 and the smaller 700bp band is the product from pB5-55 + 4 and pB3-20,22,22 and 23.

4ul of ExoSAP-IT (USB) was added to each amplicon to rid each one of excess primer and dNTP. The amplicons were incubated at 37°C for 20 minutes and then at 80°C for 20 minutes.

Sequencing reactions for exons 2, 3 and 4 were prepared for each sample using the following mix of reagents:

DYEnamic ET Terminators	2ul
DYEnamic ET Terminator Dilution Buffer	2ul
Water	3ul
Sequencing Primer	1ul
ExoSAP-IT treated PCR product	2ul
10ul total reaction volume	

The sequencing reactions were cycled in a PE 9700 thermal cycler under the following conditions, with the first three steps being performed for 25 cycles:

95°C	20 sec
50°C	15 sec
60°C	60 sec
4°C	Infinite

Ethanol precipitation was used to remove excess terminators and precipitate out the sequencing products.

The precipitated products were run on an ABI 3100 capillary sequencer.

The Electropherograms are shown in figures 2A-2D.

[0061] The present primers and kits can have any or all of the components described herein. Likewise, the present methods can be carried out by performing any of the steps described herein, either alone or in various combinations. One skilled in the art will recognize that all embodiments of the present invention are capable of use with all other appropriate embodiments of the invention described herein. Additionally, one skilled in the art will realize that the present invention also encompasses variations of the present primers, configurations and methods that specifically exclude one or more of the components or steps described herein.

[0062] As will be understood by one skilled in the art, for any and all purposes, particularly in terms of providing a written description, all ranges disclosed herein also encompass any and all possible subranges and combinations of subranges thereof. Any listed range can be easily recognized as sufficiently describing and enabling the same range being broken down into at least equal halves, thirds, quarters, fifths, tenths, etc. As a non-limiting example, each range discussed herein can be readily broken down into a lower third, middle third and upper third, etc. As will also be understood by one skilled in the art all language such as "up to," "at least," "greater than," "less than," "more than" and the like include the number recited and refer to ranges which can be subsequently broken down into subranges as discussed above. In the same manner, all ratios disclosed herein also include all subratios falling within the broader ratio.

[0063] One skilled in the art will also readily recognize that where members are grouped together in a common manner, such as in a Markush group, the present invention encompasses not only the entire group listed as a whole, but each member of the group individually and all possible subgroups of the main

group. Accordingly, for all purposes, the present invention encompasses not only the main group, but also the main group absent one or more of the group members. The present invention also envisages the explicit exclusion of one or more of any of the group members in the invention.

[0064] All references, patents and publications disclosed herein are specifically incorporated by reference thereto. Unless otherwise specified, "a" or "an" means "one or more".

[0065] While preferred embodiments have been illustrated and described, it should be understood that changes and modifications can be made therein in accordance with ordinary skill in the art without departing from the invention in its broader aspects as described herein.

Claims

What is claimed is:

1. A primer set comprising:

primers that are capable of amplifying all human leukocyte antigen (HLA) alleles of an HLA locus; and

a control primer pair that will produce an HLA control amplicon of predetermined size from the one or more HLA alleles if the one or more HLA alleles are present in the sample, wherein the portion of the HLA allele amplified by the control primer pair is common to all or substantially all HLA alleles, wherein the portion of the HLA allele amplified by the control primer pair comprises a portion of exon 4 of the HLA A locus or HLA B locus, wherein the HLA control amplicon is about 500 base pairs in length and further wherein the one or more HLA alleles are common to a single HLA locus.

PRIMERS, METHODS AND KITS FOR AMPLIFYING OR DETECTING HUMAN LEUKOCYTE ANTIGEN ALLELES

ABSTRACT

[0066] The present invention describes primer pairs, methods and kits for amplifying, identifying and/or detecting HLA alleles.

FIGURE 1

PCR

Electrophoresis/ Agarose Gel

**Hands on Time
1 hour**

ExoSap-IT

**Walk Away Time
7 hour**

Sequencing Reactions

Gel Loading Preparation

Electrophoresis/Sequencer

Analysis

FIGURE 1A

DR Group Specific SBT

Amplification

Each of the 11 DR groups (DRB1*01, 15/16, 03, 04, 07, 8/12, 09,10, DRB3, DRB4, DRB5) is amplified with a given DNA sample.

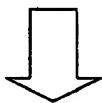


Agarose Gel

A separation, such as on an agarose gel, is performed and only those products that are positive will be taken further. (SSP).

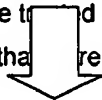
*Minimum amount of products = 1 (e.g. DRB1*0101)

*Maximum amount of products = 4 (e.g. DRB1*0301,0701, DRB3*0101, DRB4*0101).



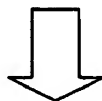
ExoSap-IT

All positive products have unused primers removed, such as with ExoSap-IT, and the template product is diluted 1:1.5 with water due to the fact that there is so much product.



Sequencing Reactions

1 or 2 sequencing reactions (forward and reverse) are done for each positive product.

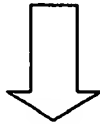


Excess Terminator Removal

Excess terminators are removed either by ethanol precipitation or by column purification.

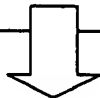


Products are resuspended and denatured for gel/capillary loading.



Samples are run on the sequencer.

The data collection program on the ABI (slab gel or capillary). Sample identification, voltage, run time, etc. are all controlled by this program.



Analysis

After the run is complete, the Sequencing Analysis program is opened and each sample is loaded into the sample manager and analyzed automatically by the software. Each product (forward and reverse) is analyzed and any bases that the software called incorrectly are corrected.



Allele Assignment

Once all electropherograms are corrected, they are put through typing software (MatchMaker, NCBI, etc) for allele assignment.

Table A Locus

			Amount/rxn	Molarity
pa5-3	HLA-A	AmpPrimer	0.5ul	20uM
pa3-29	HLA-A	AmpPrimer	0.5ul	20uM
pa5-5	HLA-A	5' Amp primer	0.5ul	20uM
pa3-31	HLA-A	3' Amp Primer	0.5ul	20uM
pa3-29-2	HLA-A	Amp Primer	0.5ul	20uM
A 3' UT			0.5ul	20uM
Aex2F-2	HLA-A	seq primer	1ul	3uM
Aex2R-4	HLA-A	seq primer	1ul	3uM
Aex3F-2	HLA-A	seq primer	1ul	3uM
Aex3R-3	HLA-A	seq primer	1ul	3uM
Aex4F	HLA-A	seq primer	1ul	3uM
Aex4R-4	HLA-A	seq primer	1ul	3uM

CAGACSCCGAGGATGGCC
 GCAGCGACCACAGCTCCAG
 ACC AGA AGT CGC TGT TCC CTY YTC AGG GA

 AAA GTC ACG GKC CCA AGG CTG CTG CCK GTG
 TCACRGCAGCGACCACAGCTCCAG

 GCCTTTTCAGAAACAAAGTCAGGGTTC

 GCCTCTGYGGGGAGAAGCAA
 GGATCTCGGACCCGGAGACTGT
 CCCGGTTTCATTTTCAGTTTAGG
 ATTCTAGTGTGGTCCCAATTGTCTC
 GGTGTCCTGTCCATTCTC
 CAGAGAGGGCTCCTGCTTTC

A Locus Multiplex Amplification Primers

pa5-3 HLA-A 5' AmpPrimer CAGACSCCGAGGATGGCC
 pa5-5 HLA-A 5' Amp primer ACC AGA AGT CGC TGT TCC CTY YTC AGG GA
 pa3-31 HLA-A 3' Amp Primer AAA GTC ACG GKC CCA AGG CTG CTG CCK GTG
 pa3-29-2 HLA-A 3' Amp Primer TCACRGCAGCGACCACAGCTCCAG

Table B Locus

					Location	Amount/rxn	Molarity
pB3-24	HLA-B	3' Amp Primer	GGT KCC CAA GGC TGC TGC AGG GG		intron 3, 1234-1256	0.5ul	20uM
pB5-48	HLA-B	Amp.	GAA CCG TCC TCC TGC TGC TCT C		Exon 1 base 20-41	0.5ul	20uM
pB5-49	HLA-B	Amp.	GAA CCG TCC TCC TGC TGC TCT G		Exon 1 base 20-41	0.5ul	20uM
pB3-20	HLA B rev	3' Amp Primer	ATC ACA GCA GCG ACC ACA GCT CCG AT		exon 5, 968-994	0.5ul	10uM each
pB3-21	HLA B rev	3' Amp Primer	ATC ACA GTA GCG ACC ACA GCT CCG AT		exon 5, 968-994		
pB3-22	HLA B rev	3' Amp Primer	ATC ACA GTA GCA ACC ACA GCT CCG AT		exon 5, 968-994		
pB3-23	HLA B rev	3' Amp Primer	ATC ACA GCA GCG ACC ACA GCG ACC AC		exon 5, 968-994		
pB5-55+4	HLA-B	5' Amp Primer	GGCTCTG ATT CCA GCA CTT CTG AGT CAC TTT AC		intron 3, 1308-1340	0.5ul	20uM
pB5-52	HLA-B	5' Amp primer	GAC CAC AGG CTG GGG CGC AGG ACC CGG		intron 1, 122-148	0.5ul	20uM
pB5-53	HLA-B	5' Amp primer	GAC CAC AGG CGG GGG CGC AGG ACC TGA		intron 1, 122-148	0.5ul	20uM
pB5-44	HLA B	5' Amp	ACGCACCCACCCGGACTCAGAA		5' untranslated, -39 to -18	0.5ul	20uM
pB5-45	HLA B	5' Amp	ACGCACCCACCCGGACTCAGAG			0.5ul	20uM
B 3' UT	HLA B	3' Amp	AGAGGCTCTTGAAGTCACAAAGGGGA		3'untranslated, 2913-2938	0.5ul	20uM
yB2F-6a+10	HLA-B	SEQ Primer	ATTA TGA TTA AG CCC CTC CTC RCC CCC AG		Intron 1 (~189-201)+nonsense bases	1ul	3uM
yB2F-5a	HLA-B	SEQ Primer	CA GCC CCT CCT TGC CCC AG		Intron 1 (~189-201)		
yB2F-6a	HLA-B	SEQ Primer	AG CCC CTC CTC RCC CCC AG		Intron 1 (~189-201)		
yB2F-7a	HLA-B	SEQ Primer	AG CTC CTC CTC GCC CCC AG		Intron 1 (~189-201)		
yB2F-12a	HLA-B	SEQ Primer	AG CCC CTC CTC GCC CCC AG		Intron 1 (~189-201)		
yB2R-4	HLA-B	Seq. Primer	GGA GGG GTC GTG ACC TGC G				
yB3F-2a	HLA-B	seq.	GGG GAC GGG GCT GAC C				
yB3F-2b	HLA-B	seq.	GGG GAC TGG GCT GAC C				
yB3F-2c	HLA-B	seq.	GGG GAC GGT GCT GAC C				
B-Ex3R	HLA-B	SeqPrimer	AAACTCATGCCATTCTCCATTC		Intron3:1100-1121		
B-Ex4F1	HLA-B	SeqPrimer	GTACATGGGTGGTCCCTA		Intron3:1494-1511		
yB4R-3	HLA-B	Seq Primer	GGCTCCTGCTTCCCTGAGAA		Int4 1871-1891		

Table C Locus

C Intron 3 R	GCAGTGGTCAAAGTGGTCA
C Intron 3 F	GCAGCTGTGGTCAGGCTGCT
C 3' UT	GGACACGGGGGTGRGCTGTCTSTC
C5ApUTG	CAG TCC CGG TTC TGA AGT CCC CAG T
C5ApUTA	CAG TCC CGG TTC TAA AGT CCC CAG T
C5X1_I1GG	GGG CCG GTG AGT GCG GGG TT
C5X1_I1TA	GGG CCT GTG AGT GCG AGG TT
C5X1_I1TG	GGG CCT GTG AGT GCG GGG TT
C3ApX5A	AGC TCC AAG GAC AGC TAG GAC A
C3ApX5T	AGC TCC TAG GAC AGC TAG GAC A
C173ApX5	GAC AGC CAG GAC AGC CAG GAC A
C3ApI4T	GTG AGG GGC CCT GAC CTC CAA
C3ApI4C	GTG AGG GGC CCT GAC CCC CAA
C3ApI4TAC	GTG AGG GGC CCT TAC ACC CAA
CAPExon5R2	GCC ATC ACA GCT CCT AGG ACA GCT A
CAPExon5R3	GCC ACC ATA GCT CCT AGG ACA GCT A
CAPExon5R4	GTG ACC ACA GCT CCA AGG ACA GCT A
CAPExon5R5	AGC TAG GAC AGC CAG GAC AGC CA
CAPExon5R1	CCA CCA CAG CTC CTA GGA CAG CTA
pC5-2	CAG TCC CGG TTC TRA AGT CCC CAG T
C5x21	GGA GCC GCG CAG GGA GG
c5x22	GGG TCG GGC GGG TCT CAG
c3x21	GGC CGT CCG TGG GGG ATG
c3x22	TCG KGA CCT GCG CCC CG
c5x31	TTC RGT TTA GGC CAA AAT CCC CGC
c5x32	GTC RCC TTT ACC CGG TTT CAT TTT C
c3x31	GCT GAT CCC ATT TTC CTC CCC TCC
c5x41	AGG CTG GCG TCT GGG TTC TGT G
c5x42	CCR TTC TCA GGA TRG TCA CAT GGG C
c5x43	CAA AGT GTC TGA ATT TTC TGA CTC TTC
c3x41	AGG ACT TCT GCT TTC YCT GAK AAG

Table DR Loci

DRB Group Specific Primers

GSDR-01	5'-TGTA AACGACGGCCAGTCACG TTTCTTGTGGSAGCTT-3'
GSDR-15/16	5'-TGTA AACGACGGCCAGTTTCC TGTGGCAGCCTAAGA-3'
GSDR-03/11/13/14	5'-TGTA AACGACGGCCAGTCGTT TCTTGGAGTACTCTACGTC-
GSDR-04	5'-TGTA AACGACGGCCAGTCGTT TCTTGGAGCAGGTTAAAC-
GSDR-07	5'-TGTA AACGACGGCCAGTTTCC TGTGGCAGGGTAAGTATA-
GSDR-08/12	5'-TGTA AACGACGGCCAGTCGTT TCTTGGAGTACTCTABGGG-
GRDR-09	5'-TGTA AACGACGGCCAGTGTTC CTTGAAGCAGGATAAGTT -
GSDR-10	5'-TGTA AACGACGGCCAGTCACA GCACGTTTCTTGGAGG-3'
GSDR-B3	5'-ACAGCTCCAGYGAWCACYAG-3'
GSDR-B4	5'-TGTA AACGACGGCCAGTAGCG AGTGTGGAACCTGATC-3'
GSDR-B5	5'-TGTA AACGACGGCCAGTGCAG CAGGATAAGTATGA-3'
GSDR-3' Universal	5'-CAGGAAACAGCTATGACCGCTY ACCTCGCCKCTGCAC-3'
CRP 1	5'-TCATGCTTTTGGCCAGACAG-3'
CRP 3	5'-GGCGGACTCCCAGCTTGTA-3'

DR Single Tube Amplification Primers

OTDR-01	TGTA AACGACGGCCAGTCCCACAGCACGTTTCTTGTG
OTDR-02/07	TGTA AACGACGGCCAGTCCCACAGCACGTTTCTTGT
OTDR-03/5/6/08/12	TGTA AACGACGGCCAGTTTACAGCACGTTTCTTGGAGTAC
OTDR-04	TGTA AACGACGGCCAGTTACTAATCACGTTTCTTGGAGCAGG
OTDR-09	TGTA AACGACGGCCAGTTCCACAGCACGTTTCTTGA
OTDR-10	TGTA AACGACGGCCAGTTACTAATCACGTTTCTTGGAGGAGG
OTDR-3-2	CAGGAAACAGCTATGACCCRYGCTYACCTCGCCKCTG

Sequencing Primers for both DR Methods (Group Specific and Single Tube)

M13 Forward	5'-TGTA AACGACGGCCAGT-3'
M13 Reverse	5'-CAGGAAACAGCTATGACC-3'

DR Single Tube Amplification Primers

OTDR-01	DRB1	5' Amp Primer	TGTA AACGACGGCCAGTCCCACAGCACGTTTCTTGT
OTDR-	DRB1	5' Amp Primer	TGTA AACGACGGCCAGTCCCACAGCACGTTTCTT
OTDR-	DRB1	5' Amp Primer	TGTA AACGACGGCCAGTTTACAGCACGTTTCTTGT
OTDR-04	DRB1	5' Amp Primer	TGTA AACGACGGCCAGTTACTAATCACGTTTCTTGT
OTDR-09	DRB1	5' Amp Primer	TGTA AACGACGGCCAGTTCCACAGCACGTTTCTTGT
OTDR-10	DRB1	5' Amp Primer	TGTA AACGACGGCCAGTTACTAATCACGTTTCTTGT

FIGURE 2A

A Locus exon 2 forward

160 170 180 190 200
C A T C G C A G T G G G C T A C G T G G A C G A C A C G C A G T T C G T G C G G T T C G

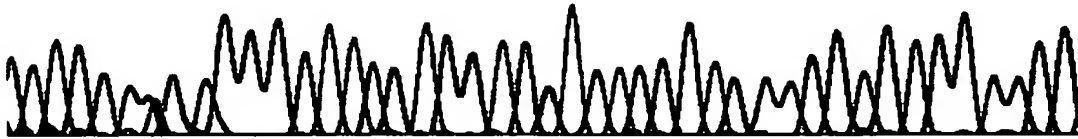


FIGURE 2B

A Locus exon 2 reverse

40 350 360 370 380
T C G C A G T G G G C T A C G T G G A C G A C A C G C A G T T C G T G C G G T T C G A



FIGURE 2C

B Locus Exon 2 Forward

190 200 210 220
A C C G G A A C A C A C A G A T C T V C A A G R C C H A S R C A C A G A C T G A C C G A G

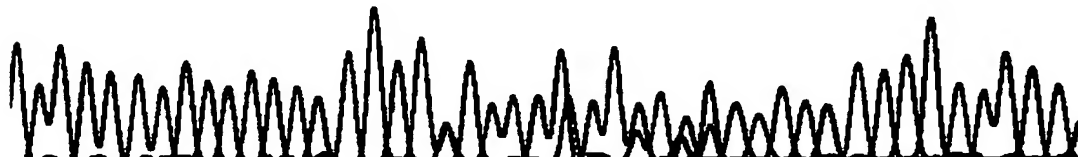


FIGURE 2D

B Locus Exon 2 Reverse

290 300 310 320
C C G G A A C A C A C A G A T C T V C A A G R C C H A S R C A C A G A C T G A C C G A G



SeCore™

POWERFUL HIGH RESOLUTION TYPING

PEPPER

SeCore™ DESIGN CRITERIA

- ▣ Specific & Robust Chemistry
- ▣ High Resolution and Low Ambiguity
- ▣ Maximized Coverage of Alleles & Polymorphism
- ▣ Reliable Detection of Alleles and Polymorphism
- ▣ Flexible Throughput
- ▣ Ease of Use
- ▣ Compatible to Various Laboratory Instruments

PEPPER

SeCore™ PCR

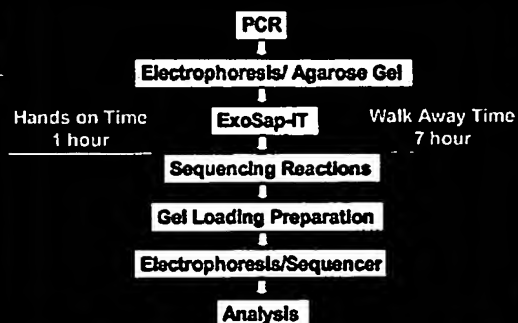
- ▣ Carefully Positioned Target Specific Primers
- ▣ Internal Control Eliminates False Negatives
- ▣ FastStart Taq DNA Polymerase
- ▣ Robust Buffer Condition – NO ALLELE DROP OUT

SeCore™ SEQUENCING

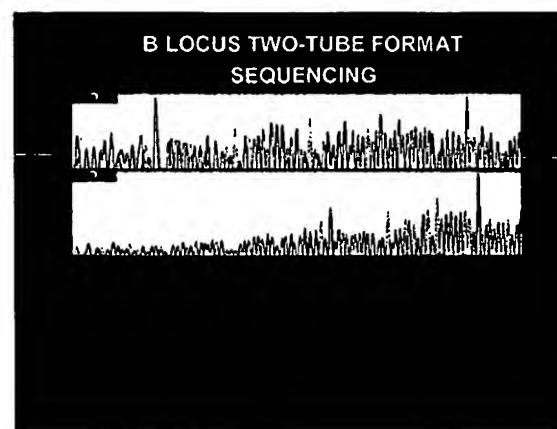
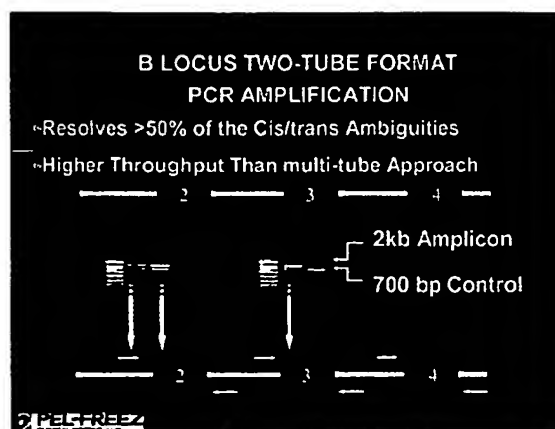
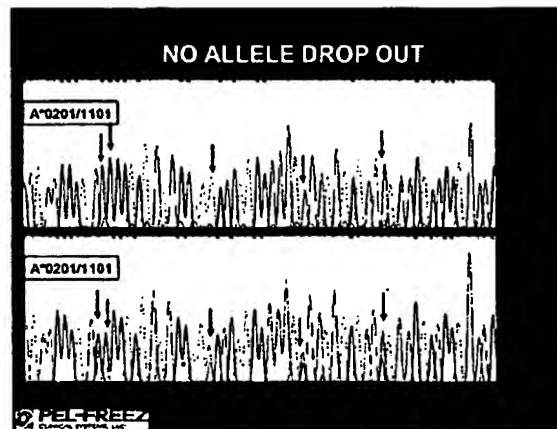
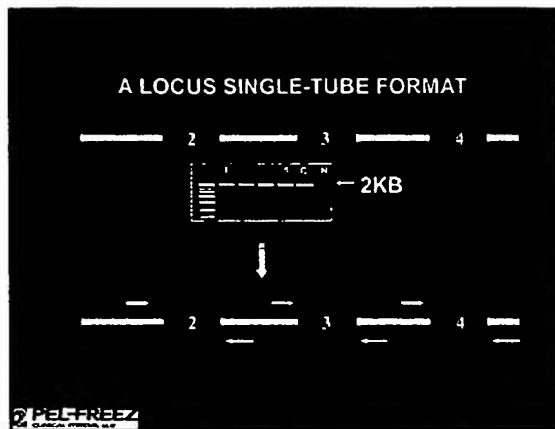
- ▣ Optimized DYEnamic™ ET Terminator Sequencing Chemistry
- ▣ Specific Sequencing Primers
- ▣ Appropriate Peak Intensity
- ▣ Robust Buffer Condition – NO ALLELE DROP OUT
- ▣ Clean Signals Generated in Proximity to Primer

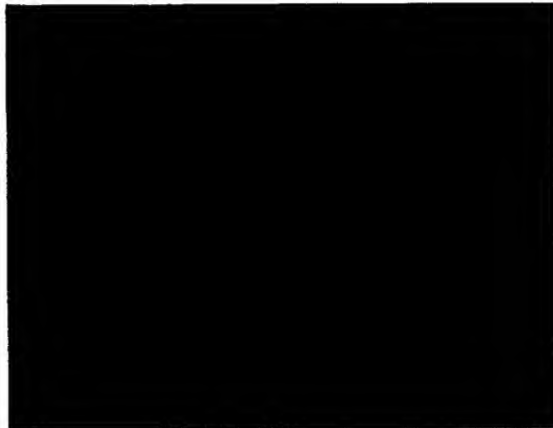
PEPPER

SeCore™ PROCEDURE



PEPPER

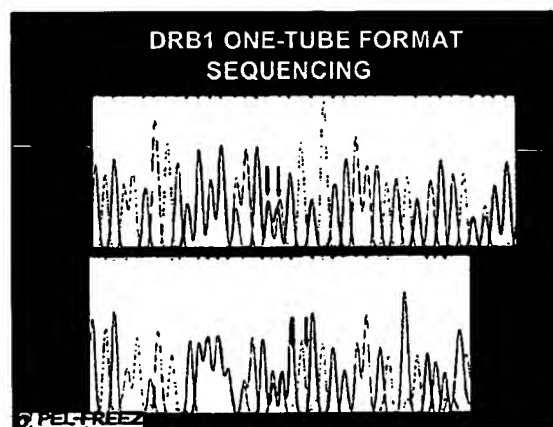




DRB1 ONE-TUBE FORMAT

- Specific Amplification in Multiplex Format
- Virtually Identical Amplification Efficiencies From All Groups
- Wide Dynamic Range of Target DNA
- Minimal Effect With Variable Volume & Amount of dNTP

SeCore™



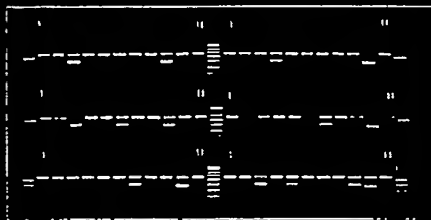
SeCore™ DRB1 GROUP SPECIFIC FORMAT

DRB1*01
 DRB1*03/11/13/14
 DRB1*04
 DRB1*07
 DRB1*08/12

DRB1*15/16

SeCore™

DRB1 GROUP SPECIFIC FORMAT PCR AMPLIFICATION



Internal Control (600bp)

PELFREEZ

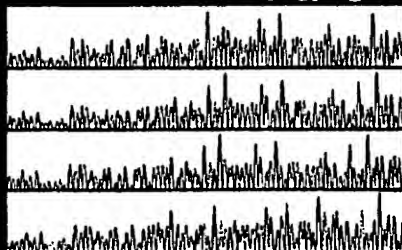
DRB1 GROUP SPECIFIC FORMAT SEQUENCING



PELFREEZ

SOLVING DRB1 CODON 86 AMBIGUITY

Sequencing Primer Distinguishes G Vs. T at
Codon 86 From the Original DR Amplicon



PELFREEZ

Compatible to Various ABI Genetic Analyzers
ABI377

One electropherogram

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POWERFUL HLA CLASS I & CLASS II SEQUENCING PRODUCTS

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Your Sequence Based Solution

Sequence Based Typing

Powerful high resolution HLA Sequencing Products from Pel-Freez Clinical Systems, LLC.

- Common sequencing protocol for all loci
- DYEnamic™ ET Terminator Chemistry
- Compatible with both capillary and slab gel systems

Class I

A Locus
B Locus

Single amplicon sequencing exon 2, 3 and 4
Dual amplicon sequencing exon 2, 3 and 4

Resolves >50%
of dis Ambiguities

Class II

DR Group

Eleven group specific amplifications
achieves the highest resolution of DRB1,
DRB3, 4 and 5 exon 2

Amplification
Internal Control

DRB1 Locus
Codon 86

Single amplicon sequencing exon 2
Target specific GT sequencing mix to
identify one of the two sample alleles
from the original DR amplicon

Slab Gel Module

Membrane combs and their companion solutions provide an extremely
simple method for sample loading the ABI 377XL

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The SeCore™ Line

Item Code	Product Name	Number of Tests
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53100-25	SeCore™ B Locus Sequencing Kit	25
53200-25	SeCore™ Cw Locus Sequencing Kit	25
53300-25	SeCore™ DRB Group Sequencing Kit	25
53310-25	SeCore™ DRB1 Locus Sequencing Kit	25
53396-25	SeCore™ DR Codon 86 Sequencing Kit	25
53400-25	SeCore™ DQB1 Sequencing Kit	25
54000-1	SeCore™ Slab Gel Sequencing Module	

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Table 1

5' Untranslated Consensus Comparisons

A Locus	CARRAGCAGAGGGGTACAGGGCGAAGTCCCAGGGCCCCAGCGTGGCTCTCAGRGTCCTCAGGGCCCCGAAGGGGGTGTATGGATTG GGGAGTCCCAGCCTTGGGGATTCCCCAACTCC GCAGTTT
B Locus	GATCAGGACGAAGTCCCAKGSCCC GGRCGGGGCTCTCAGGGTCTCAGGCTCCGAGRRCKYGYTGTCAWTGGGGAGGCGCAGC TGGGGATTCCCC ACTCCCMMSGAGTTT
C Locus	RATCAGGACGAAGTCCC GGCGGGGYTCTCWGGGTCTCARGCTCCMAGGCCGTGTCTGCAYTGGGGAGGCGCMGCGTTRAGGATTCTCYCC ACTCCCCTGAGTTT
E Locus	CAAAGTGCTGAGATTACAGGCGTGAGCCACCGCGCCAGCCAGGACTAATTTCTAAGAGTGTGCAGAGATACCGAAACCTAAAA GTTTAAGAACTGCT GATTGCTGGGAACTCTGCAGTT
F Locus	GGGAGGGGAGGGCAAGTCCCAGGGCCCCAGGAGTGGCTCTCAAGGGCTCAGGGCCCCCGA GGCGGTCTCTGGGGTTGGGAGGCT CAGTATTGAGAATTCCCCCATCTCCCCAGAGTTT
G Locus	TGAGACAGAACGCTTGGCACAGAGTAGCGGGGTACAGGGCGAAGTCCCAGGGCCTCAAGCGTGGCTCTCAGGGTCTCAGGGCCCC ACAGCGGTGTATGGRRTGGGGAGGCCCCCGGTGGGGA
H Locus	CAGGAGGAGCGGGGTACAGGGCGAAGTCCCAGGGCCCCAGCGTGGCTCTCAGGGTCTCAGGGCCCCGAAGGGGGTGTATGGATTG GGGAGGCCCGCCTTGGGGATTGCGCCACCTCC GCAGTTT
J Locus	AGGAGGAGCGGGGTACAGGCGAAGTCCCAGAGCCCCAGGCATGGCTCTCAGGGTCTCAGGGCCCCGAAGCGGTGCATGGGCTGG GGAGGTGCAGCATTGGGGATTCCCCCATCTCCGCAGAGCCC
K Locus	AGGAGGAGCGGGGTACAGGGCGAAGTCCCTATGGCCCCAGGCGTGGCTCTCAGGGTTTCAGGGCCCCGAAGCGGATGTATTGATTGG GGAGGCC AGGGTTGGGGATTCCCCCATCTCCGC AGTTT
L Locus	AGGAAAAGAGAGGTACAGGACAAAGTCCCAGGGCCCC AGCGTGGCTCTCTGGGTCTCAGGCCCCCAAGAGCGATGACTGCACTGGGGAGTCACAGGGTTGGGGATTGCCCCACTCCCC TGAGTTT

A Locus CTTTCTCCTCTSCCAACCTAYG
 TAGGTCCTTCWTCCTGGATACTACGACGGACCCAGTTCTCACTCCCATTTGGGTGTCGGGTTTCCAGAGAAAGCCAATCAGT
 GTCKTCGCGGTCCG
 B Locus CACTTCTTCTC
 CCAACYTRTGBTCGGGTCCTTCTTCCAGGATACTSGTGACGCRTCCTCCCAHTTCCCACCTCCCATTTGGGTRTYGGRTRTCTAGAGA
 AGCCAATCAGYGTGCGGBGGTCC
 C Locus CACTTCTTCTY CCAACCTGCGW
 CGGTCTCTTCTTCTTCTGAATACTCATGACGCGTCCCCAATTCCCACCTCCCATTTGGGTGTCGGRTT
 CTAGAGAAAGCCAATCAGCGTCTMCGCAGTCC
 E Locus TCCCGTTCTCTCTCGT
 AACCTGGTCATGTGTCCTTCTTCTCTGGATACTCATGACGAGACTCAGTTCTCATTTCCCAATGGGTGTCGGGTTTCTTAGAGAAAG
 C
 F Locus CTCTTTCT CTC CCAACCCGTGTCAGG
 TCCTTCTTCTGGATACTCATAAACGGCGGCCCATTTCTCACTCCCATTTGGCGTCSGTTTCTAGAGAAAGCCAATCAGTGTCCG
 CGCAGTTC
 G Locus TTCTCTCCTCCTTCTCCTAACCTGTGTC
 GGGTCCTTCTTCTCTGGATACTCACCGGGCGGCCCAAGTTCTCACTCCCATTAGGTGACAGGTTTTTAGAG
 GTCCTGG
 H Locus CT CTCTTCTCACACCTG
 CGACGGGTCTCTTTCTCTGGATACTCAGGAAGCGGGGCACAGTTCTCATTTCCCACTAGGTGTCGGGTTTCTAGAGAAAGCCAATCG
 GTGCCGCCCGCGGTCCC
 J Locus
 CTTTCTCTTCTCCTCTCCAGCCTGCGACGGGTCTTCTTCTTGACACTCACGACGGGACCCAGTTCTCACTCCCACTGAG
 TGTCCGGGTTCTAGGGAAGCCAATCAGCGTCGCGCGG
 K Locus
 CTCCTTCTCCTCTCCCAACTTATGTAGGGTCTTCTTCTTGACACTCAGGATGTGGACTCAGTTCTCACCCCCCATTTGGTGTG
 GGGTTCTAGCGAAGCCAATCGGCGTCTGGGTCC
 L Locus TGGTTCTCCCA
 CCTTCTCCTGGATACTTGTGACATAATCCCACCTTCTCACTCCCATTTGGGTGCCGGGTTTTTAGAGAAAGCCAATCAGCTTCGCC
 GCGATCCC

pA5-3
 A Locus CKSTTCTAAAGYCCGCACGCACCCACCGGGACTCAGATTCTCTCCCGAGACSCCGAGG
pB5-44 and pB5-45
 B Locus CAGTTCTAAAGTCCCCACGCACCCACCGGACTCAGARTCTCCYCAGACRCCRAG
 C 5' UT
 C Locus CCGTTCTRAAGTCCCCCAGTCAACCCACCGGACTCRSATTTCTCCCGAGSGCCGAG
 E Locus TATAAAGTCCCCA TCCGGACTCAAG AAGTTCTC
 AGGACTCAGAGGCTGGGATC
 F Locus CCAGGTTCTAAAGTCCCCACGCACCCCGGGGACTCATATTTTCCC
 AGACGGGAGGTTGGGGTC
 G Locus TTCTAAAGTCCTCGCTCACCCACCCGGACTC ATTCTCCCCAGACGCCAAGG
 H Locus GGTCTCTAAAGTCCCCACGCACCCACCGGACTCAGATTCTCCCGAGCGCCGAGG
 J Locus GGTCTCTAAAGTCCCCACGCACCCACCGGACTCGGAGTCTCCCGAGCGCCGACG
 K Locus CTGTTCCAGAAGTCCCCCGGAACCCCATTTGGGACTCAGATTCTCCCGAGCGCCGAGG
 L Locus GGACATAAGATCCCGGCACTAC AGTCCCGGGCAACCCACCGCACTCAGATTCTCCCGAAACGCCAAGG

Exon 1 Consensus Comparisons

A Locus ATG GCC RTC ATG SCK CCC CGA ACC CTC STC CTG CTA CTC TYG GGG GYY CTG GCC
 CTG ACC CAG ACC WGG GCR G
pB5-48 and pB5-49
 B Locus ATG CKG GTC AYG GMG CCC CGA ACC STC CTC CTG CTC TSG GSR GCM STG GCC
 CTG ACC GAG ACC TGG GCB G
 C Locus ATG CGG GTC ATG GCG CCC CRA RCY CTC MYC CTG CTC TCG GGA GSC CTG GCC
 CTG AYC GAG ACC TGG RCC K
 E Locus ATG GTA GAT GGA ACC CTC CTT TTA CTC YYC TCG GAG GCC CTG GCC
 CTT ACC CAG ACC TGG GCG G

F Locus	ATG GCG CCC CGA AGC CTC CTC CTG CTG CTC TCA GGG GCC CTG GCC
CTG ACC	GAT ACT TGG GCG G
G Locus	ATG GTG GTC ATG GCR CCC CGA ACC CTC TTC CTG CTR CTC TCG GGG GCC CTG ACC
CTG ACC	GAG ACC TGG GCG G
H Locus	ATG GTG CTC ATG GCG CCC CGA ACC CTC CTC CTG CTG CTC TCA GGG GCC CTG GCC
CTG ACC	CAG ACC TGG GCG C
J Locus	ATG GGG TC ATG GCG CCC CGA ACC CTC CTC CTG CTG CTC TCG GGG ACC CTG GCC
CTG GCC	GAG ACC TGG GCG G
K Locus	ATG GG GTC ATG GCG TCC CGA ACC CTC CTC CTG CTG CTC TTG GGG GCC CTG GCC
CTG ACC	GAG ACC TGG GCG G
L Locus	ATG GGG GTC ATG GCT CCC CGA ACC CTC CTC CTG CTG CTC TTG GGG GCC CTG GCC
CTG ACC	GAG ACC TGG GCC G

Intron 1 Consensus Comparisons

Aex2F-2

A Locus	GTG AGT GCG GGG TCG KG	AGG GAA ACS GCC TCT GYG GG	GAG AAG CAA SGG GCC
CKC CYG	GCG GGG RCG CAR GAC CSG GGR	AG CCG CGC	

pB5-52 and pB5-53

B Locus	GTG AGT GCG GGR TCG GS	AGG GAA ATG GCC TCT KYV GG	GAG GAG MRA GGG GAC
CGC AG	GCG GGG GCK CAG GAC CYG RGG	AG CCG CGC	

C5x1_1GG/TA/TG

C Locus	GTG AGT GCG RGG TTR GG	AGG GAA DCG GCC TCT GSG GA	GAG GAR CGA GGK GCC
CKC CCG	GCG AGG GCG CAG GAC CCG GGG	AG CCG CGC	
E Locus	GTG AGT GCG GGG TCG GG	ATG GAA ACG GCC TCT ACC GG	GAG TAG AGA GGG GCC
GGC CCG	GCG GGG GCG AAG GAC TCG GGG	AG CCG CGC	
F Locus	GTG AGT GCG GGG TCC AG	AGA GAA ACG GCC TCT GTG GG	GAG GAG TGA GGG GCC
CGC CCG	GTG GGG GCG CAG GAC TCA GGG	AG CCG CSY	
G Locus	GTG AGT GCG GGG TCA GG	AGG GAA ACR GCC CCT GCG CG	GAG GAG GGA GGG GCC
GGC CCG	GCG GGG GCG CAG GAC YCG GC	AG CCG CGC	
H Locus	GTG AGT GCA GGG TCT GC	AGG GAA ATG G TC	GAG GAG CGA GGG GCC
CGC CCG	GCG GGG GCG CAG CCA GGG	AG CCG CGC	

J Locus GTG AGT GCG GGG TCA GG AGG GAA ACG GCC TCT GCC GT GAG GAG CGA AAG GTC
CAC CTG GCT GGG GCG CAG GAC CCG GGG AG CCG CGC
K Locus GTG AGT GCG GGA TCC GG AGG GAA ATG GCC TCT GC GGG GAG GAG GT AGG GGC
CCG CGC ACT GGG GCG CAG GAC CCG GGG AG CAG CGC
L Locus GTG AGT GCG GGG TCG GG AGG GAA AGG GCC TCT GC GGG GAG AAG CGA GTG GCC
CGC CGG GC CCG GGG AG CCG CGC

A Locus CKG GAS GAG GGT CCG KYR GRT CTC ASC CAC TSC TCG YCC CCA G
yB2F-6a+10 yB2F-6-12
B Locus CCG KAG GAG GGT CKG GCG GGT YTC AGC YCC TCC TDR CYC CCA G
C Locus AGG GAG GWG GGT CCG GCG GGT CTC AGC CMC TCC TCK YCC CCA G
E Locus CCG GAG GAG GGT CCG GCC GAT CTC AGC CCC TCC TCG CCC CCA G
F Locus CCG GAG GAG GGT CTG GCG GGT CTC AGC CCC TCC TCG CCC CCA G
G Locus CCG GAG GAG GGT CCG GCG GGT CTC AAC CYC TCC TCG CCC CCA G
H Locus AGG GAG GAG GGT CCG GCG GGT CTC AGC TCC TCG CTC CCA G
J Locus CCG GAG GAG GGT CCG GCG GGT CTC AGC CCC TCC TCG CCC CCA G
K Locus AAG GAG GAG GGT CCG ACG GGT CTC AGC CCC TCC TCG CCC CCA G
L Locus CCG GAG GAG GGT CCG GCG GGT CTC AGC CTC TCC TCG CCT CCA G

Exon 2 Consensus Comparisons

A Locus GC TCY CAV TCC ATG AGS TRT TTC WHC ACH TCC RTG TCC CSG CCC GGC MGY GRR
RAG CCC CGC TTC ATC KCM GTG GGC TAC GTG GAC RAC DCG
B Locus GC TCC CAC TYC ATG AGG YAT TTC BAC ACC KCY RTG TCC CGG CCY GKC CGC GGR
GAG CYC CSC TTC ATY DCM GTG GGC TAC GTG GAC GRC ACS
C Locus GC TCC CAY TCC ATG ARG TRT TTC KHC ACM KCY GTG TCC YGG CCY RGC SSC GGR
GAG CCC CRC TTC ATC KCA GTG GGC TAC STG GAC GAC ACR
E Locus GC TCC CAC TCC TTG AAG TAT TTC CAC ACT TCC GTG TCC CGG CCC GGC CGC GGG
GAG CCC CGC TTC ATC TCT GTG GGC TAC GTG GAC GAC ACC

F Locus GC TCC CAC TCC TTG AGG TAT TTC AGC ACC GCT GTG TCG CGG CCC GGC CGC GGG
 GAG CCC CGC TAC ATC GCC GTG GAG TAC GTA GAC GAC ACG
 G Locus GC TCC CAC TCC ATG AGG TAT TTC AGC GCC GCC GTG TCC CGG CCC GGC CGC GGG
 GAG CCC CGC TTC ATC GCC ATG GGC TAC GTG GAC GAC WCG
 H Locus GC TCC CAC TCC ATG AGG TAT TTC TAC ACC ACC ATG TCC CGG CCC GGC CGC GGG
 GAG CCC CGC TTC ATC TCC GTC GGC TAC GTG GAC GAT ACG
 J Locus GC TCC CAC TCC ATG AGG TAT TTC AGC ACC GCC GTT TCC TGG CCG GGC CGC GGG
 GAG CCC AGC TTC ATT GCC GTG GGC TAC GTG GAC GAC ACG
 K Locus GT ACC CAC TCC ATA AGG TAT TTC AGC ACC GCC GTG TCC CGG CCG GGT CGC GGG
 GAG CCC CGG TAC ATC GCA GTG GGC TAC GTG GAC GAC ACG
 L Locus GC TCC CAC TCC TTG AGG TAT TTC AGC ACC GCA GTG TCC CAG CCC GGC CGC GGG
 GAG CCC CGG TTC ATC GCC GTG GGC TAC GTG GAC GAC ACA

A Locus CAG TTM GTG CMG TTB GAC AGC GAC GCC GSG AGC CRG ARG ATG GAG CYG YGG GCR
 CCG TRG ATR GAG CRG GAG RRK CCK GAG TAT TGG GAC SDG
 B Locus CWG TTS GTG MGG TTC RAC AGC GAC GCC RCG AGT OMR AGR RNG GMK MCS CSG GCG
 CCR TGG RTR GAG CAR GAG GGG CCD GNR YWT TGG GAS SVG
 C Locus CAG TTC GTG CRG TTC GAC AGC GAC GCC GCG AGT CCR AGA GGG GAG CCG CGG GMG
 CSG TGG GTG GAG MAG GAG GGG CCG GAG TAT TGG GAC CGG
 E Locus CAG TTC GTG CGC TTC GAC AAC GAC GCC GCG AGT CCG AGG ATG GTG CCG CGG GCG
 CCG TGG ATG GAG CAG GAG GGG TCA GAG TAT TGG GAC CGG
 F Locus CAA TTC CTG CGG TTC GAC AGC GAC GCC GCG ATT CCG AGG ATG GAG CCG CGG GAG
 CCG TGG GTG GAG CAA GAG GGG CCC CAG TAT TGG GAG TGG
 G Locus CAG TTC GTG CGG TTC GAC AGC GAC TCG GCG TGT CCG AGG ATG GAG CCG CGG GCG
 CCG TGG GTG GAG CRG GAG GGG CCV GAG TAT TGG GAA GAG
 H Locus CAG TTC GTG CGG TTC GAC AGC GAC GCC GCG AGC CAG AGG ATG GAG CCG CGG GCG
 CCG TGG ATG GAG CGG GAG GGG CCG GAG TAT TGG GAC CGG
 J Locus CAG TTC GTG CGG GTC GAC AGT GAC GCC GTG AGT CTG AGG ATG AAG ACG CGG GCG
 CCG TGG GTG GAG CAG GAG GGG CCG GAG TAT TGG GAC CTA
 K Locus CAG TTC GTG CGG TTC GAC AGC GAC GCC GCG ACT CCG AGG ATG TAG CCG CAG TCG
 CCG TGG TTG GAG CAG GAG GGA CCG GAG TAT TGG GAC CGG
 L Locus GAG TTC GTG CGG TTC GAC AGC GAC TCC GTG AGT CCG AGG ATG GAG CCG CGG GCG
 CCG TGG GTG GAG CAG GAG GGG CTG GAG TAT TGG GAC CAG

A Locus	VAS ACA SGG MAW RTG ARG GSC CAS	TCA CAG RBT VAY CGA GHG RRC CTG SRG AYC
SYG CDC	SGC TAS TAC AAC SAG AGC GAG GMC G	
B Locus	RAS AYA CRG AHS WNS AAG VBC HMS	RCR CRG RCT KRC MGA GWG RRC YTG CGS AHS
SYG CKC	SVC BAC TAC AAC CAG AGC KAG GMC G	
C Locus	GAG ACA CAG AAS TAC AAG CGC CAG	GCA CAG RCT GAC CGA GTG RRC CTG CGG AAM
CTR CGC	GGC TAC TAY AAC CAG AGC GAG GMC R	
E Locus	GAG ACA CGG AGC GCC AGG GAC ACC	GCA CAG ATT TTC CGA GTG AAY CTG CGG ACG
CTG CGS	SGC TAC TAC AAT CAG AGC GAG GCC G	
F Locus	ACC ACA GGG TAC GCC AAG GCC AAC	GCA CAG ACT GAC CGA GTG GCC CTG AGG AAC
CTG CTC	CGC CGC TAC AAC CAG AGC GAG GCT G	
G Locus	GAG ACA CGG AAC ACC AAG GCY CAC	GCA CAG ACT GAC AGA ATG AAC CTG CAG ACC
CTG CGC	GGC TAC TAC AAC CAG AGC GAG GCC A	
H Locus	AAC ACA CAG ATC TGC AAG GCC CAG	GCA CAG ACT GAA CGA GAG AAC CTG CGG ATC
GCG CTC	CGC TAC TAC AAC CAG AGC GAG GGC G	
J Locus	CAG ACA CTG GGC GCC AAG GCC CAG	GCA CAG ACT GAC CGA GTG AAC CTG CGG ACC
CTG CTC	CGC TAC TAC AAC CAG AGC GAG GCG G	
K Locus	AGC ACA CGG AAC ATC AGG CCC GCG	CAC AGA CTG ACA AGA GTG AAC CTG CCC ATG
CCG CGC	CGC TAC TAC CAC CAG AGC TAG GCC G	
L Locus	GAG ACA CGG AAC GCC AAG GGC CAC	GCG CAG ATT TAC CGA GTG AAC CTG CGG ACC
CTG CTC	CGC TAT TAC AAC CAG AGC GAG GCC G	

Intron 2 Consensus Comparisons

Aex2R-4

A Locus	GTGAGTGACCCCRSCCSGGGGCGCAGGTCASGAC	CYCTCATCCCCC
ACGGACGGGCCRGGTSRCCCA	CAGTCTCGGGGTCCGAGATCCRCCCC	GAAG CCGCGGGRCYCCG

yB2R-4

B Locus	GTGAGTGACCCCGCCYGGGGCGCAGGTCACGAC(CCC)	CCCCAWCCCCS
ACGKACGGCCSGGCTCKCCYC	GAGTCTCYRGGTCCGAGATCCGCCYCCCYGAGG	CCGCGGGGACCC G

C Locus GTAGTGACCCCRGCCCCGGGGCGCAGGTCMCGACCCC TCCYCATCCCC
 ACGACGGCCCGGTCGCCYM RAGTCTCCSS TCTGAGATCCWCCCC RAGG(TGGAT)CTGCGGAACCC G
 E Locus GTAGTGACCCCGGCCAGGGAGCAGGTACGACCCC TCCCCATCCCCC
 ACGACGGCGGGTCCCCTC GAATCTTCGGGTCCCAGATTACCCC AAG GCTGCGGAACCC G
 F Locus GTAGTGAMCCCGGCCGGGGCGCAGGTACGACC
 ACCSCCATCCGYACGGACGCCCGGGTCCCYCM GAGTCTCGGATCCGAAATCTACCCC GAGG
 CAGCGGA CCC G
 G Locus GTAGTAACYCCGGCCACAGGCMGAGATCACGACCCCCACCTCCATGCCCC
 ACGACGSCCGGTACTCC GAGTCTCGGGTCTGGGATCCACCCC GAGG CCGCGGACCC G
 H Locus GTAGTGACCCCGGCCGGGACGACGAGTCAGACCCCTCCCC ATCCCC ACGGAGGG
 CCGGTCGCCCTC GAGTCTCTGGTCCGAGATCCTCCCC GAAA CCGCGGACC
 J Locus GTAGTGACCCCGGCCGGGGCGCAGATCACTTACTCCCCGCTCCATGCCCTC ACGGACGGCCCTGGTCCCCCT
 GAGTCTCCGGTCCAAGATCGACCCC GAGG CTGCGGGACCT G
 K Locus GTGAATGACCCCGCCTGGGGCGAAGTCAAGATCCACCCC GAGG CTGCGGGACCC G
 ACGACGGCCGGTCCCCCGCGAGTCTCGGCTCCAAGATCCACCCC GAGG
 L Locus GTAGTGACCTTGCCCGGGCGCAGGTACGATCCCTCCCATCCCCC
 ACGACAGCCAGTCCCGGTCTGAGTCTCCGG TCTGAGATCCACCCC GAGG CTGCGGGACCT G

AEX3F-2

A Locus
 AGACCTTGHCCCCGGAGAGGCCAGGGCCCTTWACCCGGTTTCATTTTCAGTTTAGGCCAAAAATYCCCCCRGGTTGGTYGGG
 GCBGR CRGGC TYGGGG ACYGGGCTGAC

yB3F-2a/b/c

B Locus CCCARACCTCGACCCGRMGAGAGCCCCAGGCRCSTTTACCCGGTTTCATTTTCAGTTGAGGYCAAAA
 TCCCCGGGGTTGTCGGGGGGG CGGGC(GGGC)TCGGGG(G)ACKGKGTGAC
 C Locus CCCAGACCTCGRCCGGAGAGAGCCCYAGTCRCCTTACCCGGTTTCATTTTCRGTTAGGCCAAAA
 TCCCCGGGGTTGTCGGGRCCTGGGGGGG TCGSGG ACBGGGCTGAC
 E Locus CCCAGACCTAGACCCGGGAGAGTCTCAGCGCCCTTACCCGG TTCTTTTCAGTTTAGGCCAAAA
 TGCCACAGGTGTGGCGACGGGGGGGG TTGGTG GCGGACTGAC
 F Locus CCCAGACCTCCACCCGGGAGAGTCCAGGCGCCTTACCSAGGTTTCATTTTCAGTTTAGGCCAAAA
 TCCCCGGGGTTGGCGGGAGGGGGGGG TAGCTG GCGGGGCTGAC

G Locus CCCAGACCCCTCTACCTGGGAGAACCCAGGCGCCTTTACC AAAA
 TCCYCGGGTGGTCCGGGCGAGGCGAGGC TCGGTGG GCGGGGCTGAC
 H Locus CCGAGACCCCTTGACCTGGGAGAGGCCCGCCTTTACCCGGTTTCATTTTCAGTTTAGGCCAAAA
 TCCCGCGGGTTGGTCGGGGC AGGCGGGGC TCGGGGG ACCGGGCTGAC
 J Locus CAGAGATCCTCGACCCGGGAGAGCCCGCCCTTTACCTGGTTTCATCTTCAGTTGAGGCCAAAA
 TCTCCGAGGTTGCTAGGKCCGGGCCAGGGC TCGGTGG GCGGGGCTGAC
 K Locus CCAGATCCTCGACCCGGGAGAGGCCCGCCTTTACCAGGTTTCATTTCCGTTTAGGCCAAAA
 TCCCGCGGGTTGGTCGGGGCGGGGCGGGGC TCGGTGG GCGGGGCTGAC
 L Locus CCCAGACCCCTCGACCAAGGAAGAACTCGGGCGCCTTTACCCGGTTAAATTCAGTTTAGGCCAAAA
 TCCCGCGGGTTGGTCGGGGCGGAGCGGGGC TCGGTGT TCGGGGCTGAC

A Locus KYGGGGTCSRGGCCAG
 B Locus CCGRGS CKRGCCAG
 C Locus CRCGGGSCGGGCCAG
 E Locus TAAGGGCGGGGCCAG
 F Locus TCGGGGACCGGCTAG
 G Locus CGARGGGTGGGCCAG
 H Locus CGC GGGGCGGGCCAG
 J Locus CGCGGAAC TGGGCCAG
 K Locus CGCGGGGCGGGGCCAG
 L Locus GCGGGGCGAGGCCATG

Exon 3 Consensus Comparisons

A Locus
 B Locus
 C Locus
 E Locus GG TCT CAC ACC CTG CAG TGG ATG CAT GGC TGC GAG CTG GGG CCC GAC RGG CGC
 TTC CTC CGC GGG TAT GAA CAG TTC GCC TAC GAC GGC AAG GAT
 F Locus
 G Locus GT TCT CAY ACC CTC CAG TGG ATG ATT GGC TGC GAC CTG GGG TCC GAC GGW CGC
 CTC MTC CGC GGG TAT GAA CAG TAT GCC TAC GAT GGC AAG GAT

H Locus GT TCT CAC ACC ATG CAG GTG ATG TAT GGC TGC GAC GTG GGG CCC GAC GGG CGC
TTC CTC CGC GGG TAT GAA CAG CAC GCC ACG CAG AAG ATT CAT
J Locus GG TAT CAC ATC CTC CAG GGA ATG TTT GGC TGC GAC CTG GGG CCC GAC GGG CGT
CTC CTC CGC GGG TAT GAG CAG THT GCC TAC GAC GGC AAG GAT
K Locus
L Locus

A Locus
B Locus
C Locus
E Locus TAT CTC ACC CTG AAT GAG GAC CTG CGC TCC TGG ACC GCG GTG GAC ACG GCG GCT
CAG ATC TCC GAG CAA AAG TCA AAT GAT GAT GAT GCG GCG GAG
F Locus
G Locus TAC CTC GCC CTG AAC GAG GAC CTG CGC TCC TGG ACC GCA GCG GAC ACT GCG GCT
CAG ATC TCC AAG CGC AAG TGT GAG GCG GCC AAT GTG GCT GAA
H Locus GCT CTG AAC GAG GAC CTG CGC TCC TGG ACC GCG GCG GAC ATG GCA GCT
CAG ATC ACC AAG CGC AAG TGG GAG GCG GCC CGT CAG GCG GAG
J Locus TAC ATC GCC CTG AAC GAG GAC CTG CGC TCC TGG ACC GCC GCG GAT ACC GCG GCT
CAG ATT ACC CAG CGC AAG TAT GAG GCG GCC AAT GTG GCT GAG
K Locus
L Locus

A Locus
B Locus
C Locus
E Locus CAC CAG RGA GCC TAC CTG GAA GAC ACA TGC GTG GAG TGG CTC CAC AAA TAC CTG
GAG AAG GGG AAG GAG ACG CTG CTT CAC CTG G
F Locus
G Locus CAA AGG AGA GCC TAC CTG GAG GGC ACG TGC GTG GAG TGG CTC CAC AGA TAC CTG
GAG AAC GGG AAG GAG ATG CTG CAG CGC GCG G

H Locus CAG CTG AGA GCC TAC CTG GAG GGC GAG TTC GTG GAG TGG CTC CGC AGA TAC CTG
 GAG AAC GGG AAG GAG ACG CTG CAG CGC GCG G
 J Locus CAA AGG AGA GCC TAC CTG GAG GGC ACC TGC ATG GAG TGG CTC CGC AGA CAC CTG
 GAG AAC GGG AAG GAG ACG CTG CAG CGC GCG G
 K Locus
 L Locus

Intron 3 Consensus Comparisons

Aex3R-3

A Locus GTACCRGGGGCCACGGGGCGCCTHCCTG
 ATCGCCTRTAGRTCTCCCGGGCTGGCCTCCACAAAGGAGGGGAGACAAATTGGGACCAACACTAGAATATCRCCCTCCCTCTGGT
 CCTGAGGGGAGAGG

B-Ex3R

B Locus GTACCAGGGGCAGTGGGGAGCCTTCCCC
 ATCTCCTATAGRTCGCCSGGATGGCCTCCMACGAGAAGRRGAGGAAATGRGAKMAGCGCTAGAATGTGCCCCTCCSTTGAAT
 GGAGAAATGGCATG
 C Locus GTACCARGGGCAGTGGGGAGCCTTCCCY
 ATCTCCYRTAGATCTCCCGSATGGCCTYCCACGAGGAGGGGAGGAAATGGGATCAGCRCTRGAATATCGCCCCCTCCCTTGAAT
 GGAGAAATGGSATG
 E Locus GTAAGAGGGTCCACAGGGCTACTCTCCC
 ATCTCCTTCTTGGGCTAGGACTGTGCCCCACAGCTGACAGACCTCAAACAGTAGAAGAAACAGGGATGGAGGCCAGAATACCACT
 CCTCCCTTGGATC

F Locus GTACCAGGGGCCAT GGGCGCCTTCCCT
 ATCTCCTGTAGATCTCTTGGGATGGCCTCGCACAAAGTTGGGAGGAAAGTGGRCCCAATGCTAGGATATCGCCCCTCCCTCTAGT
 CCTGAGTAGGAAG
 G Locus GTACCAGGGGCAGT
 GGGGGCCTCCCTGATCTCCTGTAGACCTCYCAGCCTGGCCTAGCACAAAGGAGAGGAGGAAATGGGACCAACACYAGAATATC
 GCCCTCCCTCTGGTCTGAGGGAGAG
 H Locus GTACCAGGGGCCACAGGG
 CGCCTCCCGGATGGCCTGTAGATCTCCGGGCTGGCCTCCACAAAGAAAGGAGACAAATGGGACCAACACTATAATATCGCCC
 TCCCTCTGGTCTGAGGAGAG
 J Locus GTACCAGGGGCCAT
 GGGAGCCTGCTCGATCTCCTGTAGATCTCCCCGGGCTGGCCTCGCACAAAGGAGGGGAAGAAATGGAAMCACCACCAGAAATATC
 GCCCTCCCTCCTGTCTGACGGAGAG
 K Locus GTACCAGGGAACACAA
 GACGCCTCCCTGATCGCCTGTAGATCTCCTGGGCTGGCTTCCACAAAGAGAGAGGAAATGGGACCAACACTAGAAATGTCTGT
 CCTCTCTGTGTCCTGAGGGAGAG
 L Locus
 GTACCAGGGGCCACGGGGCGCCTCCCTCATTTCTCTGTAGATTTCCCGGGCTGGCCTCCACAGGAGAGTAGGAAAAATGGGAC
 CAATGCTAGAATATCGCCCTCCCACTGGTCTCTGAATGGGAAG

A Locus AATCCTCCTGGGTTTCCAGATCCTGTACCAGAGAGTGACTCTGAGGTTCGSGCCTGCTCTSTGAC
 WCAATTAAAGGGATAAAATCTCTGAMGGARTGACSGRAAGACGA TCCCTCGAATACTG
 B Locus AGTTTCTCTGAGTTTCC
 CCCCCTCTKCTSTCTAG (G) ACAATTAAAGGRATGACRCTCTGTAGGAAATGKAGGGGAAGACAGTCCCCTAKRATASTG
 C Locus AGTTTCCYAGTTTCC
 ACAATTAAAGGATGAAGTCYTTGAGGAAATGAGGGGAAGACAGTCCCTRGAATACTG
 E Locus AGGAGAGGAGCTGTCACCTGAGGTACAGGAGATCCTATACCAAGAGTGACTCTCTTAAA
 GGGCAGACCTCTCTCAGGGGCAATTAAGGAATCTAGTCTCGCTGGAGATTCATCCTTCAGAT
 F Locus AATCTTCTGGCTTTCGAGATCCGGTACCAGAGAGTGACTGTGAGAGTCCGCCCTGCTCTCT
 GGGACAATTAAAGGATGAATYCTGAGGGAATGGAGG AAGACAGTCCCCTGGAATACCGATC
 G Locus AATCCTCTGGGTTTCCAGATCCTGTACCAGAGAGTGATTTCTGAGGYYCCGTCCTGCTCTCT
 GGGACAATTAAAGGATGAAGTCTCTGAGGAGTGAGGGGAAGACAATCCCTGGARGACTGATC
 H Locus AATCCTCTGGGTTTCCA
 GAGAGTGACTCTGAGGGTCCGCCGCTGCTCTT
 GACACAATTAAAGGATGAATCTCTGAGGAAATGAAGG AAGACAATCCCTGGAATACTGATG

J Locus
AATCCTCCTGGGTTTCCAGATCCTGTATCAGAGATTGACTCTGAGGGCCCCACCCCTGCTCTTCTCTGGGACAATTAAGGGATGAAG
TCTCTGAGGGAGTGGAGGGGAAGACAAATCCCTGGAAGACTGATC

K Locus
AATCCTCCTGGGTTTCCAGATCCTGTACAAAGAGAGTACTCTGAGGGTCTGCCCCCTGCTCTC
TGATACAATTAAAGGATGAAATCTCTGAGGAAATGAAGG AAGACAATCCCTGGAATACTGATG

L Locus
AATCCT GGGTTTCCAGATCCTGTACCAGAGAGTAACCTCTGAGAGCCACCCCTGCTCTC
TGGGACAATTAAAGGATGAAGTCCCTGAGGAAATGGAGGAGAGACAGTCCCTGGAATACTGATC

A Locus
ATGASTGGTTCCCTTTGA (CACA) CACMGGCAGCAGCCTT GGGM
CCGTGACTTTTCCCTCAGGCCCTGTTCTCTGCTTCACACTCAATGTGTGGGGTCTGAGTCCAGCAC

B Locus
ATCAGGKGTCCTTTGA CCC CTGCAGCAGCCTT
GGMACCCTGACTTTTCTCAGGCCCTTGTCTCTGCTGCCYCACACTCAGTGTGTTGGGCTCTGATTCCAGCAC

C Locus
ATCAGGGGTCYCCCTTTGA CCACCTTGACCACCTGCRGAGCTGTGGTCAGGCTGC TGACCTTTC
TCTCAGGCCCTTGTCTCTGCCTSAYRCTCAATGTGTTRAAGTTTGAYTCCAGCTT

E Locus
GAACCTGATGAGCAGTTCTCTTT
GACTCCCAGTATTAGGAATCACGGGGAGTTTCTCTCGTGCCTGATTCTCAGCCCCACACCAAGAGTTTTTTGGAGGTCTGACTC

F Locus
CGCGTCCCCCTTTGAGCCCTCCAACAGCCTTGGGCCCCCGTGACTTTTCTC
TCAAGTTTGTCTCTGCCCTCACACTCAATGTGTTTGRGGCTCTGATTCCAGTCCCTCGGCCCTCCACTTAGGTCA

G Locus
AGGGTTCCCTTTGACCCC ACAGCAGCCTTGGCACCCAGG ACTTTTCCCC
TCAGGCCCTTGTCTCTGCCCTCACACTCAATGTGTGGGGTCTGACTCCAGTCCCTCTGAGTCCCTTTGGC

H Locus
AGTGGTTCCCTTTGACACTGGCAGCAGCTTGGG CCGGTG
ACTTTCCCTCAGGCCCTTGTCTCTGCTTCACACTCAATGTGCCCTGGGGTCTGAGTCCAGCTCTTCTGAGTCCCT

J Locus
CGCGTCCCCCTTTACCCCC ACAGCAACCTTGGGCACCCAGG
ACTTTCCCTCCCGGCCCTTGTCTCTGCCCTCACACTCAATGTGTC GGAGTCTGACTCCAGCTCCCTCTGAGTCCCTTTGGC

K Locus
AGGGTTCCCTTTGACACCAGCAGCCTTGGGCCCCGTTACTTTTCCCCCTC
AGCCCTTGTCTCTGCTTTACACTCAATGTGTGGGGTCTGAGTCCAGCTCTTCTGAGTCCCTCAGC

L Locus
CGTGGTCCCCCTTTGACCCCTTGACAGCCTGGGGCACCCAGGAATTTTCCCTCTC
AGGCCCTTGTCTCTCCCTCACACTCAGTGTGTCCGTGGCTCCGATTCCAGCTCTTCTGAGTGCCTTTGGC

pa5-5

A Locus TTCTGAGT CYYTCA GCCTCCACTCAGGTCAGGACCAGAAAGTCGGTGTTCCTTCCCTYYTCAGGGA
(CTAGAATTTTCCACGGA)ATAGRAGATTATCCCAAGTGCCTGTGTCCAGGCTGGTGCTCT
B Locus TTCTGAGTCACTTTA CCTCYACTYAGATCRGGAGCAGAACTCYCTGTTCCTCCRCCTCAGAGA
CTCGAACTTTTCCAATGA ATAGGAGATTATCCCAAGTGCCTGYRTCCAGGCTGGTGTHT
C Locus TTHTGAGTY CTK CR GCCTCCACTCAGGTCAGGACCAGAAAGTCGGTGTTCCTCCCTCAGAGA
CTAGAACTTTTCCAAWGA ATAGGAGATTATCCCAAGTSCCTGTGTCCAGGCTGGCGTCT
E Locus
AGCATCCACACAGGCCAGGACCAGAAATCCCTTTTACACCTTCTACCTGGGCTAGCTCATCCCGATTCTAGAAC
TTTCCAAGGA ATAAGAGGCTATCCAGATCCCTAAGTCCAGGCTGGTGTC
F Locus GGGCCAGAAGTCCCTGCTCCCTCCVCTCAGAGACTCKAACTTTCCAAGGAATAGGAGAT
TTTCCCAGGTGTCGT GTCCAGGCTGGTGCT
G Locus CTCCACTCAGGTCAGAAACCRGAGGTCCCTGCTCCCCCGCTCAGAGA
CTAGAAC TTTCCAAGGAATA GGAGATTATCCCAAGTGCCCGTGTCCAGGCTGGTGCT
H Locus CAGCCTCCACTCAGGTCAGGACCAGAAAGTCGGTGTTCCTCCTCAGGACTAGAA
TTTTCACGGAATA GGAGTTTATCCCAAGTTCGTGTCCAGGCTGTTGTCT
J Locus CTCCACTCAGATCAGG CCAGAASTCCCTGCTACCCCTGCTCAGAGA
CTAGAAC TTTCCAAGGAATA GGAGATTATCCAGGCGCTGTGTCCAGGCTRGTTCT
K Locus CTCCACTCAGGTCAGGACCAGAAAGTCACTG TTCCCTCCTCAGGGA
CTGGAATTTTCCACGGAATTCGGAGATTATCCAGATACCTGTGTCCAGGTTGGTGCT
L Locus CTCCACTCAGGTCAGGACCAGAAAGTCCCTGCTCCCC CATCAGAGA
CTCGAACTTTTCCAAGGAATA GGAGATTATCCAGATTCCCTGTGTCCAGGCTGGTGCTCT

Aex4F

A Locus GGGTTCTGTGTCYCTTCCCCATCCCRGGTGTCT GTCCATTCTCAAGATRGCCACATGYR TGCTGG W
GGAGTGTCCTACACAGATSSAAAATGCCCTGAATKWTCTGACTCTTCCYG WSAG
B Locus GGGTTCTGTG YCCCTTCCCCACMCCAGGTGTCT GTCCATTCTCAGGCTGGTCACATGGG TGGTCCTA
GGGTGTSYATGARAGAT GCAAAGCGCCTGAATTTTCTGACTCTTCCCCATCAG

B-Ex4F1

C Locus GGGTCTGTGCCSCCTTYCCYACCCAGGTGTCCT GTCRRTTCTCAGGATRGTCACATGGG CRCTGYT
 GGAGTGTCSCAAGAGAGAT RCAAAGTGCTGAATTTTCTGACTCTTCCCRCTCAG
 E Locus AGGTTTGTCCCTCTTCTCCT ACTATAATTGTCCTCTTCC TTCTCAGGATGGTCACATGGG TGCTGCT
 GGAGTGTCCTCATGAGAGAT ACAAAGTGCCTGAATTTTCTGACTCTTCCCTCAG
 F Locus GGGTCTGTGCTCCCTTCCCAACCCAGGTGTCCTG TCCAKTCTCAGGTTGGTCACATGGG TGCTGCT
 GGGTTTCCCATGAGGAGT GCAAAGTGCCCTGAATTTTCTGACTCTT CTCAG
 G Locus GGGTCTGTGCTCCCTTCCCAACCCAGGTAT CTGGTTTCATTCTTAGGATGGTCACATCCAGGTGCTGCT
 GGAGTGTCCTCATGAGAGAT GCAAAGTGCTTGARTTTTCTGACTCTTCCCTTCAG
 H Locus GGGTCTGTGCTCCCTTCCCAACCCAGGCTCCT GTCCATTCTCAAGATGGCCACATGCG TGCTGGT
 GGAGTGTCCTCATGACAGAT GCAAATGCTGAATTTTCTGACTCTTCTCTGTCAG
 J Locus GGGCTCTGTGCTCCCTTCCCAACCCAGGTGTCCTA TTCATCAGGATGGTCACATGGGCGC TGCTGG
 GG TGTCCCATGAGGAAT GCAAAGTGCTGAGTTTTCYGACTCTTCCCTTCAG
 K Locus GGGTCTGTGCTCCCTTCCCAACCCAGGTGTCCT GTCCATTCTCAGGATGGCCACATGCG TGCTGCT
 GGAGTGTCCTCATGAGAGAT GCAAAGTGCTGAATTTTCTGACACTTCTCTGTTAG
 L Locus GGGTCTGTGCTCCCTTCCCAACCCAGGTGTCCT GTCCATTCTCAGGATGGTCACATGTA TGCTGCT
 GGAGTGTCCTATGAGGAAT GCAAAGTGCTGAATTTTCTGACTCTTCCCTCAG

Exon 4 Consensus Comparisons

Intron 4 Consensus Comparisons

		Aex4R-4															
A Locus	KTA	AGG	AGG	GAG	AYG	GGG	GTG	T	CAT	GTC	TYT	TAG	GGA	AAG	CAG	GAG	CC
TC TC T						GG(AG)AC	CTT		TAG		CAG						
B Locus	GTA	AGG	AGG	GGG	ATG	AGG	GGT		CAT	ATC	TST	TCT	CAG	GGA	AAG	CAG	CCC
T TC(T						GG	AG	CC	CTT	C)AG	CAG						
C Locus	GTA	AGG	AGG	GGR	ATG	RGG	GGT		SAY	RTS	TCT	TMT	CAG	RGA	AAG	CAG	TCC
T (TC T)						GG	AG	CC	CTT	C	AG	CYR					

yB4R-3

K Locus		GG	TCG	GTG	CTG		GGG	GCT	GAG		GGT	CAG	GGA	CGC	TCA
CCT TCC CCT	TTT	TTC	CCA	G											
L Locus		GG	CA	GGG	CTG		AGG	CCT	GGG		GGT	CAG	AAC	CCC	TCA
CCT CC CTC T	CCT	TTC	CCA	G											

Exon 5 Consensus Comparisons

A Locus YTT	AG	CYR	TCT	TCC	CAG	CCC	ACC	RTC	CMC	ATY	GTG	GGC	ATC	MTT	GCT	GGC	CTR	GTT	CTC
B Locus CTW	AG	CCR	TCT	TCC	CAR	TCC	ACC	RTC	CCC	ATC	GTG	GGC	ATT	GTT	GCT	GGC	CTG	GCT	GTC
C Locus CTG	RG	CCR	TCT	TCC	CAG	CCY	ACC	ATC	CCC	ATC	RTG	GGC	ATC	GTT	GCT	GGC	CTG	GCT	GTC
C 170* CTG	AG	CCG	TCT	TCC	CAG	CCC	ACC	ATC	CCC	AAC	TTG	GGC	ATC	GTT	TCT	GGC	CCA	GCT	GTC
E Locus CTT	AG	CCG	GCT	TCC	CAG	CCC	ACC	ATC	CCC	ATC	GTG	GGC	ATC	ATT	GCT	GGC	CTG	GTT	CTC
F Locus CTT	AG	CAG	TCT	CCC	CAG	CCC	ACC	ATC	CCC	ATC	GTG	GGC	ATC	GTT	GCT	GGC	CTT	GTT	GTC
G Locus CTT	AG	CAG	TCT	TCC	CTG	CCC	ACC	ATC	CCC	ATC	ATG	GGT	ATC	GTT	GCT	GGY	CTG	GTT	GTC
H Locus CTT	AG	CCA	TCT	TCC	CAG	CCC	ACC	ATC	CCC	ATC	GTG	GGC	ATC	GTT	GCT	GGC	CTG	GTT	CTA
J Locus CTT	AG	CCC	TCT	CCC	CAG	CCC	ACC	ATC	CCC	ATT	GTG	GGT	ATC	ATT	GCT	GGC	CTG	GTT	CTC
K Locus CTT	AG	CAG	TCT	TCT	CAG	CCC	ACC	ATC	CCC	ATC	GTG	GGT	ATC	GTT	GCT	GGC	CTG	GTT	CTC
L Locus CTT	AG	CCG	TCT	TCT	CAG	CCC	ACC	ATC	CCC	ATC	GTG	GGC	ATC	GTT	GCT	GGC	CTG	TTT	CTC

A Locus	GSA GCT RTG RTC RCT GGA GCT GTG GTC GCT GCY GTG AKG TGG AGG ARG AAG
AGC TCA G	
B Locus	GTG GYM RYY GTR GYY RTS GKM GCT GTG GTC GCT RCT GTG RTG TGT AGG AGG AAG
AGY TCW G	
C Locus	
AGC TCA G	
C 170*	
GTG ATA C	
E Locus	
AGC TCA G	
F Locus	
AGC TCA G	
G Locus	
AGC TCA G	
H Locus	
AGC TCA G	
J Locus	
AGC TCA G	
K Locus	
AAC TCA G	
L Locus	
AGC TCA G	

Intron 5 Consensus Comparisons

A Locus
 GTGGRG (TG) AAGGRTGAARGGTGGGGTCTGAGATTTCTTGCTCTCACTGAGGGTTCCAAGMCCCAGSTAGAARTGTGCCCTGY
 CTCRTTACTGGGAAGCACCCDYCCACAATYATGRGCCKACCC
 B Locus GTAGGG
 AAGGGGTGAGGGGTGGGGTCTGRGTTTYSSTTGTCCTCCACTGGGGGTTTCAAGCCCCAGGTAGAAAGTGTTCCTCCCTGCMTCATTACTG
 GGAAGCAGCATSCACACA GGGGCTAAYGC
 C Locus GTAGGG
 AAGGGGTGARGAGYGGGGTCTGGGTTTCTTGTYCCACTGGGAGTTTCAAGCCCCAGGTAGAAAGTGTGCCCCRCCTYGTTACTG
 G AAGCACCATCCACAC Y TGGGCCATCCC
 E Locus GTGGGG AAGGGA
 GAAGGGTGGGGTCTGAGTTTCTTGTCCTCCACTGGGGTGTTCAGCCCCCTAGGTAAAGTGTGTCTCCTGCCTCGTTACTGGGAAGCA
 CCATCCACACACAGAGCCTACCC
 F Locus GTAGG
 AAGGGGTGAGGAGTGGAGTCTGAGTTTCTTGTCCTCCACTGGGGGTTGCAAGCCCCCAAGTAGAAAGTGTGCCCCTGCCCTCATTACTG
 GGAAGCACCATCCACACTCATGGGTCTACCC
 G Locus GTAAGG
 AAGGGGTGACAAAGTGGGGTCTGAGTTTCTTGTCCTCCACTGGGGGTTTCAAGCCCCAGGTAGAAAGTGTGCCCCTGCCCTGGTTACTG
 GGAAGCACCATCCACACTCATGGGCCTACCC
 H Locus
 J Locus GTGGGG
 AAGGGGTGAGGAGTCGGGTTTGAGTTTCTTGTCCTCCACTGGGGGTTTCAAGCTCCAGGTAGAAATGTGTCTGCTGGTTACCG
 GGAAGCACCATCCACATTTCATGGGCCTACCC
 K Locus
 L Locus

 A Locus AGYCTGGG CCCTGTGTGCCAGCACTTACTCTTTTGTAAAGCACCTGTK
 AMAATGAAGGACAGATTTATCACCTT GATTAYRGCRCGTGATGGGACCTGATGCCAGCAGTCACAAGTCACAGGGG
 B Locus AGMCTGGGACCCTGTGTGCCAGMACTTACTCTTTTGTGCAGCACATGTG
 ACAATGAARSAYRGATGTATCRCCTTTRRTGGTGTGGGTTCCTGATTYCAGCATTCATGAGTCA GGGG
 C Locus
 AGCCTGGGACCCTGTGTGCGYAGCACTTACTCTKTTGTGAAGCACATG (TG) ACAAYGAAGGACRGATGTATCACCTT
 GATGATTATGGTGTGGGGTCCTTGATTCCAGCATTCRTGAGTCAGGGG

E Locus

AGCCTGGGGCCCTGTGTGCCAGCACCTACTCTTTTTTTTTTGGACGGAGTCTTGGCTCTGTCAACCCAGGCTGGAGTGCAATGGC
GTGGTTTCAGCTCACTGCAACCTCCGCCTCCCAGGTTCAA

F Locus

AGCCTGGG CCCTGTGTGCCAGCACCTACTCATTTGTAARGCTCCTG TG

AAAATGAAGGACAGATTCTTCAC TTCGATGATTATGGTGGTGATGGG ACCTGATCCCAGCAGTCACAAAT

G Locus

AGCCTGGG CCCTGTGTGCCAGCACCTTCTCTTTTGTAAAGCACCTG TG

ACAAATGAAGGACAGATTATACACCTT GATGATT GTAGTGATGGGACCTGATCCTAGTAATCAC

H Locus

AGCCTGGG CCCTGTGTGCCAGCACCTTACTCTTTTGTA GCACCTG TG

ACAAATGAAGGACAGATTCTCACCTT GATGATT GTAGTGATGGGATCTGACCCAGTAATCAC

K Locus

L Locus

A Locus

AAGTCCC TGAGS

ACAGACYTCAGGAGGCKRRTTGGTCCAGGRCCCACAYCTGCTTTCTTCATGTTTCTGTATCCYGCCCTGGGTCTGCAGTCACAC

ATTTCTGGAAACT

B Locus

AAGTCCCCTGCTAAGG

ACAGACCTTAGGAGGCGAGTTGGTCCAGGACCCACACTTGCTTTCCCTYGTGTTTCCCTGATCCTGCCYTGCGTCTGTAGTCATAC

TTCTGGAAATT

C Locus

AAGTCCCCTGCTAAGG

ACAGACCTTAGGAGGCGAGTTGSTYCACGRACCCACARCTGCTTTCCCYRTGTTTCCCTGATCCTGCCCTGGGTCTGCAGTCTC

TAGTTCTGGAAACT

E Locus

GCAATTCTCCTGCCCTCAGCCTCCCTAGTAGCTGGGACTACACATGCGTGCCACCACACCTGGCTAATTTTTTTTTGTATTTT

TAGTGGAGATGGGGTTTCACTATGTTGGCCAGGCTGGTCTCGAACT

F Locus

CACAGGGGAAGTCCCCTGCTGATG

ACAGACCTCAGGAGGCGAGTTGGTCCAGGACCCACATCTGCTTTCTTCATATTTCTTGATCCTGCCCTGGATCTACAGTTACAC

TTTTCTGGAAAC

G Locus

AGGTCAGGGGAAGTCCCTGGCTAAGGACAGACCTTAGGAGGCGAGTTGGTCGAGGACCCACATCTGCTTTTCCTTGTTTTTCCT

GATCCCGCCCTGAGTCTGCAGTCACACATTTCTGGAAC

H Locus

J Locus AGGTCAGGGGAAGGTCCTGCTGA
GGACAGACCTTAGGAGGGCAGTTGGTCCAGGACCCACATCTGCTTTCCTTGTTTYTCCTGATCCTGCCCTTGGTTGCAGTCAC
ACATTTCTGGAAAC
K Locus
L Locus

A Locus
TCTCTGRGGTCCAAGACTWGGAGGTTCCCTCTAGGACCTTAAGGCCCTGRCTCYTTTCTGGKATCTCACAGGACATTTTCTTCYC
ACAG

B Locus
CCTTTTGGKTCCAAGACKAGGAGGTTCCCTCTAAGATCTCATGGYCCTGCTTCCCTCCAGTSCCCTCACAGGRCAATTTCTTCCC
ACAG

C Locus
TCTCTGGGTCCAAGACTAGGAGGTTCCCCCTAAGATYRCATGGCCCTGMCTCCTCCCWGTCCCCCTCAYAGGGCAATTTCTTCCC
ACAG

E Locus
CCTGACTTTGTGATCTGCCCTCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGTGGTGAGCCACCGCACCCAGCCGACCTACTCT
TTTGTAAGCACCTGTGACAATGAAGGACAGATTATCACCT

F Locus
TTCTCTGGGATCAAAGACTAGGGGTTTGCTCTAGGACCTTATGGCCCTGCCCTCCTTTCTGGCCTCTCACAGGACATTTCTTCC
CATAG

G Locus
TTCTCGAGGGTCCAAGACTAGGAGGTTCCCTCTAGGACCTCATGGCCCTGCCACCTTTCTGGCCTCTCACAGGACGTTTCTTCC
CACAG

H Locus
J Locus
TTCTCRAGGTTCCAAGACTAGGAGGTTCCCTCTAGGACCTCATGGCCCTGCTACCTTCTGGCCTCTCACAGGACGTTTCTTCC
CGCAG

K Locus
L Locus

A Locus
B Locus

C Locus
E Locus
TGACGATTGTGGTGTGGGACCTGATCCCAGCAGTCACAGGTCACAGGGGAAGTCCCTGCTGAAGACAGACCTCAGAAAGGGC
AGTTGATCCAGGACCCACACCTGCTTTCTTCACGTTTCCTG
F Locus
G Locus
H Locus
J Locus
K Locus
L Locus

A Locus
B Locus
C Locus
E Locus
ATCCTGCCCTGGGTCTGCAGTCACAGTTCAGGAAACTTCTCTGGGATCCAAAACCTAGGAGGTTCCCTCTAGGACCTTATGGCCCT
GCCTCCTCCCTGGCCCCCTCACAG
F Locus
G Locus
H Locus
J Locus
K Locus
L Locus

Exon 6 Consensus Comparisons

A Locus	WT	AGA	AAA	GGA	GGG	AGY	TAC	WCT	CAG	GCT	GCA	A
B Locus	GT	GGA	AAA	GGA	GGG	AGC	TAC	TCT	CAG	GCT	GCG	T
C Locus	GT	GGA	AAA	GGA	GGG	AGC	TGC	TCT	CAG	GYT	GCG	T
E Locus	GT	GGA	AAA	GGA	GGG	AGC	TAC	TCT	AAG	GCT	GAG	T
F Locus	AT	AGA	AAC	AGA	GGG	AGC	TAC	TCT	CAG	GCT	GCA	G
G Locus	AT	TGA	AAA	GGA	GGG	AGC	TAC	TCT	CAG	GCT	GCA	A
H Locus	AT	AGA	AAA	GGA	GGG	AGC	TAC	TCT	CAG	GCT	GCA	A
J Locus	AT	AGA	AAA	GGA	GGG	AGC	TAC	TCT	CAG	GCT	GCA	A
K Locus	AT	AGA			GTG	AGC	TAC	TCT	GAA	GCT	GCA	A
L Locus	AT	AGA	ACA	AGG	AGG	AGC	TAT	GCT	CGG	GCT	GCC	T

Intron 6 Consensus Comparisons

A Locus	GTAAGTATGAAGGAGG	MTGATSCMWGARRTCM	
	YTGGGATATTGTGTTTGGGAGCC	CRRTGGGGAGCYCAMCCA	CCYCACAATTCTCTCTTAGCCACATSTTCTGTGGGATCT
	GACCAGGTTC		
B Locus	GTAAGTGR	TTGGGGYGGGA	GTGTGRAGGAGCT
	CACCCA	CCCCMTAATTCCTCCTGT	CMCACGTCTCCTGYGGGCTCTTGACCAGGTCC
C Locus	GTAARTGATG	SCRGYRGGC	GTGTGRAGGAGCT
	YACCYA	CYCCATAAYTCCTCTTGT	CCCACATCTCCTGCGGGCTCT GACCAGGTCTT
E Locus	GTAAGTGC		GGGCGGGAGCGT GGAGGAGCTCGCCACCCCTAT
	AATTCCTCCTGCA	CCACATCTCCTGTGGGCTCTGACCAGGTCT	
F Locus	GTAAGATGAAGGAGG	CTGATCCCTGAGATTG	
	TTGGGATATTGTG	TCAGGAGCCCTATGAGGGAGCTCACCCA	CCCCACAGTT CCTCTAGCCACAT
	CTGTGGGCTCTG	ACCAGGTCC	
G Locus	GTAAGTATGAAGGAGG	CTGATCCCTGAGATCC	
	TTGGGATCTTGTG	TTGGGAGCCCATGGGGGAGCTCACCCA	
	CCCCACAATTCTC	CTCTGGCCACATCTCCTGTGGTCTCTGACCAGGTGC	

H Locus GTAAGTATGAAGGAGGCTGATCCCTGAAATCCTTTGG
ATATTGTGTTGGAGCCCATGGGGAGCTCACCCA
CCCCACAAATTCCTCTAGCCACATCTACTGTGGGATCTGACCAGGTCC
J Locus GTAAGTATGAAGGAGGCTGATCCCTGAGATCC
TTGGGATATTGTGTTGGGAGCCCATGGGGAGCTCACCCA
CCCCACAAATTCCTCTAGCCACATCTCCTGTGGGATCTGACCAGGTTC
K Locus GTAAGTATGAAGTGGGCTGATCCCTGA TCC
TTGGGATATTGTGTCGGGAGCCCATGGGGAGCTACCCAAACCCACAGA
TTCCTCCTCTAGCCGATCTCCTCTGGGCTCTGACCAAGTCC
L Locus GTTAGTATG GGGATTAGAGGGCTGC TCCC TGAGATCGT
TGGGACAGGTAGACAAGA TTCCTCCTTTAGCCACATCTCCTGTGGGCTCTGACCAGTTCC

A Locus TGTTTTTGTYCTACCCCG
B Locus TGTTTTTGTCTACTCCA
C Locus TTTTTTTGTTCTACCCCG
E Locus TGTTTTTGTCTACCCCG
F Locus TRTTTTTGTCTACCCCAA
G Locus TGTTTTTGTCTACTCTAG
H Locus TGTTTTTATTCTACTCCAG
J Locus TTTTTTGTCTACCCCG
K Locus TGTTTTTGTCTACCCCG
L Locus TATTTTTGTTCTACCCCG

Exon 7 Consensus Comparisons

A Locus	GC AGT GAC AGT GCC CAG GGC TCT GAT RTG TCY CTC ACA GCT TGT AAA G
B Locus	SC AGC GAC AGT GCC CAG GGC TCT GAT GTG TCT CTC ACA GCT TGA AAA G
C Locus	SC AGC AAC AGT GCC CAG GGC TCT GAT GAG TCT CTC ATC RCT TGT AAA G
E Locus	GC AGC GAC AGT GCC CAG GGC TCT GAT GAG TCT C ACA GCT TGT AAA G
F Locus	TC ACT GAC AGT GCY CAG GGC TCT GGG GTG TCT CTC ACA GCT AAT AAA G
G Locus	GC AGT GAC AGT GCC CAG GGC TCT AAT GTG TCT CTC ACG GCT TGT AAA T
H Locus	GC GGC AAC AGT GCC CAG GGC TCT GAT GTG TCT CTC ACA GCG TGA AA G
J Locus	GC AGC CAA AGT GCC CAG GGC TCT GAT GTG TCT CTC ACG GCT TGT AAA G
K Locus	GC AGC GAC CAT GCG CAG GGT TCT GAT GTG TCT CTC ACG GCT TGT AAA G
L Locus	GC AGC AAT TGT GCT CAG TAC TCT GAT GCA TCT CAT GAT ACT TGT AAA G

Intron 7 Consensus Comparisons

A Locus	GTGAGAGCYTGGAGGCCCTRATGTGTGTTGGGTGTTGGYRGAACAGTGGACRCAGCTGTGCTA TGGGGTTTCTTTSCRTTGGATGTATTGAGCATGCCGAT
B Locus	GTGAGATTCTTGGGTCTAGAGTGGYRGGGKGSVKGTCTGGGKSKGRKGGGCAGWGGGAAAGGCCTGGGTAATGGRSAT TCTTTGATTGGGATGTTTCGCGTGTSTRT
C Locus	GTGAGATTCTGGGGAGCTGAAGTGGTC
K Locus	GGGGTGGGGCAGAGGGAAAGGCCTRGGTAATGGGGATYCTTTGATWGGGACGTTTCGARTGTGTGGT
E Locus	GTGAGATTCTGGGGTCTGAAGTGGGTGGAGGGTGGGGCAGAGGGGACAGGACTGGGTGTGGGGATTTTGTATTCAGAAATT TTGAGTGTGTGGTGGGCTGTTTCAGAGTGTCTATC
F Locus	GTGACACTCCAGGCAGGGGCCCTGATGTGAGTGGGTGTTGGGGGGAACAGA GGGGACTCAGCTGTGCTATTGGGTTTCTTTGACTTGGATGTCTTGAGCATGAAAT

G Locus	GTGACACCCC	GGGGGCCCTGATGTGTGGGTTGTTGAGGGV	AACAG
BGGACATAGCTGTGCTATGAGGTTTCTTTGACTTSAATGTATTGAGCATGTGAT			
H Locus	GTGAGACCTT	GGGGGCCCTGATGTGTGGGGGTGTTGGGGGGAACAG	
TGGACACAGCTGTGCTATGGGG	TTCTTTGAATTTGATGTTTGTAGCATGCCGAT		
J Locus	CTGAGACCCCT	GGGAGGCTGATGTGTGGGTTGTTGGGG	TAACAG
TGGATATAGCTGTGCTATGGGGTTTCTTTGACTTGGATGTATTCAGCACATGAT			
K Locus	GTGAGACACT	GGGGACCTGATGTG GGGGGTGTGGGGC	AATAG
TGGACGCAGCTGTGCTATGGGGTTTCTTTGAATTGGATGTATTGAGCATGTGAT			
L Locus	GTGAGACAT	GGGGGGCCCTGAAGT	GGTGGGGGTG
GGGGTT	CTCTGGATTTAGACAT		AGGCAGAGGGGACATGATTCTGTGTA

A Locus	GGGCTGTTTAAARGTGTGACYCCTCACTGTGTGAYRGATAYGAAKTTGTTTCATGAATWTTTTTCTATAG
B Locus	GGGCGTTTYAGASTGTCAATCRCTTACCATGACTAACCAAGAAATTTGTTTCATGACTGTTGTTTTCTGTAG
C Locus	GRRCYGTTTCAGAGTGTSAATCRCTTACCATGACTGACCTGAATTTGTTTCATGACTATTGTGTTCTGTAG
E Locus	ACTTACCGTGACTGACCTGAATTTGTTTCATGACTATTTTCTTCTGTAG
F Locus	GGGCTATTTAGAGTGTACCTCTCACTGTGACTGATACGAATTTGTTTCATGAATATTTCT CTATAG
G Locus	GGGCTGTTTAAAGTGTCAACCCCTCACTGTGACTGATATGAATTTGTTTCATGAATATTTT TCTGTAG
H Locus	GGGCTG CCAAAGTGTCAATCCATTACTGGACAGATATGAATTTGTTTCATGAATATTTT TCTATAG
J Locus	GGGCTGTTGAAGGTGTGACCCCTCACTGTGAGTGATATGAATTTGTTTCATGAATATTTT TCTATAG
K Locus	GGGCTGTTTAAAGTGTCAACCCCTCACTGTGACGGATATGAATTTGTTTCATGAATATTTTATTATTATAG
L Locus	

Exon 8 Consensus Comparisons

A Locus	TG TGA
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B Locus CC TGA
 C Locus CC TGA
 E Locus CC TGA
 F Locus TG TGA
 G Locus TG TGA
 H Locus TG TGA
 J Locus TG TGA
 K Locus TG TGA
 L Locus CT TGA

3' Untranslated Consensus Comparisons

A3' UT

A Locus GACAGCTGCCCTTGTGTGGGACTGAGAGGCAAG AKTTGTTCCCTGCCCT TCCCTTTGTGACTTGAAGAACC
 CT GAC TTTGTTT CTGCAAAGGCACCTGCATGTGTCTGTTCRTGTAGG

B 3' UT

B 3' UT

B Locus GACAGCTGTCTTGTGAGGGACYGAGATGCAGG ATTTCTTCAKCCCT
 CCCCTTTGTGACTTCAAGAGCCTCT GGCATCTCTTT CTGCAAAGGCACCTGAATGTGTCTGYGYCCTGTAG
 C Locus GACAGCTGCC TGTGTGGGACTGAGATGCAGG ATTTCTTCAACCT YTCC
 TTTGTGACTTCAAGAGCCTCT RGGCATCTCTTT CTRCAAAGGCAYCTGAATGYGTCTGCCGTTCCCTGTAG
 E Locus GACAGCTGCCCTTGTGTGGGACTGAGATGCACAGCTGCCCTTGTGTGGGACTGAGATGCAGGATTTCCCT
 CACGCTCCCTATGTGTCTTAGGGGACTCTGGCTTCTCTTTTGTGCAAGGGCCTCTGA
 F Locus GACAGCTTCCCTTGTGTGGGACTGAGAAGCAAG
 ATATCAATGTAGCAGAATTGCACCTGTGCCCTCACGAACATACATAAAATTTAAAAATAAAAAATATACTTTTATAGA
 TACAGGTAG
 G Locus AACAGCTGCCCTGTGTGGGACTGAGTGGCAAG(ATT GTTCATGCCT) TCCCTTTGTGACTTCAAGAACCCT
 GACTYCTCTTT STGCAGAG ACCAGCCACCCCTGTGCCCCACC
 H Locus GACAGCCGTCTTGTGTGGGACTGAGAGGCAAG ATTTGTTACACACC T TCCCTTTGTGACTTGAAGAACC
 CT GAC TTT CTGCAAAGGCACCTGAATGTGTCTGTTCCTGTAGG

J Locus GACAGCTGCCTTGTGTGGGACTGAGAGGCAAG ATTGTTTCATGCC T TCCCTTTGTGACTTCAAGAACC
CT GACTTCTCTTT CTGCAAAGGCATCTGAATGTGTCTGTGCCCTATAGG
K Locus GACAGCTGCCTTGTGTGGGACTGAGAGGCAAG ATTGTTACGGC TTCCCTTTGTGACTTCAAAAACC CT
GAC TCTCTTT CTGCAAAGGCACCTGAATGTGCCTGTGTCTCTGTAGG
L Locus CCATGTGGTAGGCTGTTACAGAGTGTCAACCAAGTACAGTGACT
GCCCTGGATTGTATGATTATTTTCTCCTAGCTTGAGACAACCTGCTTGAGTGGGACTGAGAGATACAAAAATTTCTTCA

A Locus CATAATGTGAGGAGGTGGGGAGAS Y ACCCCACCCCCCATGTCCACCATGACCC TCTTCCC
ACGCTGACCTGTGCTCCCTCCCCAATCATC TTTCCTGTTSCAGAGAGGTGGGGCTGAGG
B Locus CMTAATGTGAGGAGGTGGAGAGAC(C)AGCYCAMCYBYGTGTCCACYGTGACCCYT

C 3' UT

C Locus CATAATRTGAGGAGKTGG ASAG ACAGCYCACCCCCCGTGTCCACCGTGACCCCT
E Locus ATCTGTCT
F Locus ATATGTTTTTATAGCATGCACGTAATGTGTGTGTGTGTGTGTGTGAAGA
GAAAGAGTGAATAGAGAGATTAAAGATTCTTTTATGGTGAAAGATATACATATATTGG
G Locus
ATGACCCCTCTTCCCTCATGTGAACTGCATTCTCTTCCCCAATCACCTTTCCCTGTTCCAGAAAAAGGGGCTGGGATGTCTCCGTCTC
TGTCTCAAATTTGTGGTSCACTGAGCTATAACTTACTTCTGTA
H Locus CATAATGTGTGGAGGGGAGACCA ACCC ACCCTCATGTCCACCATGACCC
TCTTCCCCACGCTGATCTGTGTTCCCTCCCC AATCATC TTTCCTGTTCCAGAGAGCGGGGCTGAGA
J Locus CATAATGTGAGGTGGTGGGAGACCA GCCC ACACCCGTGTCCACCATGACCC
TGTTCCCACACTGACCTACATTCTTCCCCG ATCACC TTTCCTGTTCCAGAGAAGTGGTGTGGGA
K Locus CATAATATGAGGAGGTGGGAGACCA ACCC ACCCCCATGTCCACCATGACCC
TCTTCCCTCATGTGACCTGTGTTCCGTCTCCAATAATTAATCATTCCTGCTCCATAGAGGTGAGGCTGAGA
L Locus GGTCCCTCCTGTGACACACACCATTTGTAATTTAAGAGCTCCTGACTTCTATATCTGCACTT
GACACGTGAATATATCTATGTGTCTGTGTTCCAGTTAGCATAATGTGAGGAAATGGGCTACTG

A Locus TGTCTCCATCTCTGTCTCAACTTCATGGTGCACTGAGCTGTAACTTCTTCTTCCCTATTAAAA
F Locus AACTAGCCAGCTTGACTCAGTTTAGGTGATCCCAATTTTGGTGGCAACAACCAAGCATC

G Locus GAATCTGAGTATAAAATTTASTTTTTCAAATTATTTCCTCAAGAGAGATTGATDGGTTAA TTAAA
GGAGAAGATTTCCTG
H Locus TGTCTCCATCTTTTCTCAACTTTATG TGCACTGAGCTGTAACTTCTTACTTCCCCTCTTAAAAATTAGA
J Locus TGTCTCCATCTCTGTCTCAACTTCAATGGTGCACTGAGCTGTAACTTCTTACTTCCCCTATTAAA
K Locus TGTCTCCATCTCTGTCTCAACTTTATG TGCACTGAGCTGTAACTTCTTACTTCCCCTATT
L Locus GTCCACCACTGCCACCAGGACCACCCACACACTAACCTGTCTCTCTT

APPENDIX I

Anthony Nolan Research Institute EXON IDENTITIES AND AMBIGUOUS TYPING COMBINATIONS 17 January 2003

HLA-B

Sequences identical over exons 2 + 3

Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Code in table
B*0705	B*0706				B*0705/0706
B*15010101	B*15010102N				B*15010101/B*15010102N
B*1512	B*1519				alleles not present in table
B*15170101	B*15170102				alleles not present in table
B*180101	B*1817N				B*180101/1817N
B*270502	B*2713	B*270504			B*270502/270504/2713
B*350101	B*3540N	B*3542			B*350101/3540N/3542
B*390101	B*390103				B*390101/390103
B*400101	B*400102				B*400101/400102
B*40060101	B*40060102				B*40060101/40060102
B*44020101	B*4419N	B*44020102S	B*4427		B*44G1
B*47010101	B*47010102				B*47010101/47010102
B*510101	B*510105	B*5111N	B*5130	B*5132	B*51G1

Ambiguous typing combinations over exons 2 + 3

Combination 1	Combination 2	Combination 3	Combination 4
B*070201 + B*0801	B*0705/0706 + B*0807		
B*070201 + B*0812	B*0707 + B*0801		
B*070201 + B*1306	B*0731 + B*1301		
B*070201 + B*1402	B*0726 + B*1403		
B*070201 + B*140601	B*0707 + B*1405		
B*070201 + B*15010101/B*15010102N	B*0709 + B*1563	B*0707 + B*1507	
B*070201 + B*1507	B*0709 + B*1545		
B*070201 + B*1518	B*0709 + B*1510		
B*070201 + B*1539	B*0724 + B*1540	B*0726 + B*1565	
B*070201 + B*1563 B*0707 + B*1545			
B*070201 + B*180101/1817N	B*0707 + B*1814	B*0726 + B*1813	
B*070201 + B*1811 B*0731 + B*1810			
B*070201 + B*270503	B*0721 + B*270503	B*0729 + B*270503	B*070202 + B*270503
B*070201 + B*2715	B*0731 + B*2704		
B*070201 + B*350101/3540N/3542	B*0709 + B*3534	B*0724 + B*3515	B*0726 + B*3508
	B*0718 + B*3505		
B*070201 + B*3503	B*0724 + B*3533		
B*070201 + B*3504	B*0705/0706 + B*3534	B*0712 + B*3522	
B*070201 + B*3506	B*0705/0706 + B*3503		
B*070201 + B*350902	B*0726 + B*3518		
B*070201 + B*3512	B*0705/0706 + B*3539		
B*070201 + B*3527	B*0711 + B*3534		
B*070201 + B*390101/390103	B*0705/0706 + B*3915	B*0707 + B*3903	
B*070201 + B*3907	B*070203 + B*3907	B*0729 + B*3907	B*0721 + B*3907
B*070201 + B*400101/400102	B*0705/0706 + B*4033		
B*070201 + B*4002	B*0705/0706 + B*4018		
B*070201 + B*4003	B*0709 + B*4018		
B*070201 + B*40060101/40060102	B*0705/0706 + B*4044		
B*070201 + B*4011	B*0707 + B*4002		
B*070201 + B*4016	B*0705/0706 + B*4032		
B*070201 + B*4020	B*0707 + B*4003		
B*070201 + B*4033	B*0707 + B*4031		
B*070201 + B*4038	B*0709 + B*400101/400102		
B*070201 + B*4039	B*0731 + B*4002		
B*070201 + B*4102	B*4032 + B*4201		
B*070201 + B*44G1	B*0724 + B*4421	B*0720 + B*4416	
B*070201 + B*440302	B*0726 + B*4428		
B*070201 + B*4405	B*070203 + B*4405	B*0729 + B*4405	B*0721 + B*4405
	B*0730 + B*4405		
B*070201 + B*4803	B*0707 + B*4801		
B*070201 + B*51G1	B*0724 + B*5116	B*0726 + B*5129	
B*070201 + B*510201	B*0724 + B*5134		
B*070201 + B*5108	B*0725 + B*5129		
B*070201 + B*5109	B*0724 + B*5131		
B*070201 + B*5121	B*0731 + B*5116		

B*070201 + B*5123	B*0720 + B*5134
B*070201 + B*570301	B*0726 + B*5702
B*070201 + B*7801	B*0708 + B*5606
B*0703 + B*15010101/B*15010102N	B*0716 + B*1570
B*0703 + B*1503	B*0716 + B*1561
B*0703 + B*1508	B*0708 + B*151101
B*0703 + B*180101/1817N	B*0716 + B*1803
B*0703 + B*350101/3540N/3542	B*0716 + B*3529
B*0703 + B*3905	B*0716 + B*390101/390103
B*0703 + B*3913	B*0716 + B*390202
B*0703 + B*400101/400102	B*0716 + B*4043
B*0703 + B*5108	B*0716 + B*5120
B*0703 + B*780202	B*0716 + B*7801
B*0704 + B*0813	B*0726 + B*0801
B*0704 + B*1505	B*0725 + B*1539
B*0704 + B*180101/1817N	B*0725 + B*1815
B*0704 + B*270502/270504/2713	B*0725 + B*2710
B*0704 + B*350101/3540N/3542	B*0725 + B*3511
B*0704 + B*3503	B*0726 + B*3538
B*0704 + B*3524	B*0725 + B*3521
B*0704 + B*440301	B*0726 + B*44G1
B*0704 + B*4404	B*0731 + B*4421
B*0704 + B*5109	B*0725 + B*51G1
B*0704 + B*5131	B*0725 + B*5116
B*0704 + B*5301	B*0725 + B*5308
B*0704 + B*5502	B*0725 + B*5501
B*0704 + B*5802	B*0725 + B*5806
B*0705/0706 + B*350101/3540N/3542	B*0709 + B*3504
B*0705/0706 + B*3527	B*0711 + B*3504
B*0705/0706 + B*3543	B*0709 + B*3544
B*0705/0706 + B*4003	B*0709 + B*4002
B*0705/0706 + B*4020	B*0709 + B*4011
B*0705/0706 + B*4031	B*4032 + B*8101
B*0705/0706 + B*4102	B*4016 + B*4201
B*0705/0706 + B*570101	B*0709 + B*570301
B*0705/0706 + B*5704	B*0728 + B*5702
B*0707 + B*1301	B*0718 + B*1311
B*0707 + B*1562	B*0712 + B*1503
B*0707 + B*4039	B*0731 + B*4011
B*0707 + B*5104	B*0718 + B*5106
B*0709 + B*3527	B*0711 + B*350101/3540N/3542
B*0709 + B*4009	B*0717 + B*4018
B*0709 + B*4037	B*0711 + B*4002
B*0709 + B*4042	B*0717 + B*4033
B*0709 + B*44G1	B*0728 + B*4417
B*0709 + B*5301	B*0711 + B*5305
B*0709 + B*5512	B*0711 + B*5502
B*0712 + B*4018	B*0718 + B*4024
B*0720 + B*15010101/B*15010102N	B*0724 + B*1514
B*0720 + B*1550	B*0731 + B*1514
B*0720 + B*3508	B*0724 + B*3545
B*0720 + B*3515	B*0726 + B*3545
B*0720 + B*4504	B*0724 + B*4501
B*0720 + B*5001	B*0724 + B*5002
B*0720 + B*510201	B*0724 + B*5123
B*0720 + B*570301	B*0724 + B*5707
B*0720 + B*5802	B*0724 + B*5807
B*0724 + B*1544	B*0731 + B*1521
B*0724 + B*1550	B*0731 +
	B*15010101/B*15010102N
B*0724 + B*5121	B*0731 + B*51G1
B*0724 + B*5502	B*0731 + B*5601
B*0724 + B*5610	B*0731 + B*5602
B*0725 + B*1518	B*0726 + B*1551
B*0725 + B*5001	B*0726 + B*4504
B*0725 + B*5002	B*0726 + B*4501
B*0801 + B*1302	B*0802 + B*1309
B*0801 + B*140601	B*0812 + B*1405
B*0801 + B*15010101/B*15010102N	B*0804 + B*1556
	B*0812 + B*1507

B*0726 + B*5108

B*0801 + B*1504	B*0809 + B*1507	
B*0801 + B*1515	B*0804 + B*1508	
B*0801 + B*1536	B*0802 + B*1525	
B*0801 + B*1563	B*0812 + B*1545	
B*0801 + B*1564	B*0804 + B*1529	
B*0801 + B*180101/1817N	B*0812 + B*1814	B*0804 + B*1807
B*0801 + B*1806	B*0815 + B*180101/1817N	
B*0801 + B*1809	B*0802 + B*180101/1817N	
B*0801 + B*3503	B*0813 + B*3538	B*0807 + B*3506
B*0801 + B*3520	B*0804 + B*350101/3540N/3542	
B*0801 + B*3534	B*0807 + B*3504	
B*0801 + B*3537	B*0809 + B*3505	
B*0801 + B*3539	B*0807 + B*3512	
B*0801 + B*380201	B*0802 + B*3905	
B*0801 + B*390101/390103	B*0812 + B*3903	
B*0801 + B*390602	B*0809 + B*3903	
B*0801 + B*3915	B*0807 + B*390101/390103	
B*0801 + B*3927	B*0815 + B*390101/390103	
B*0801 + B*400101/400102	B*0804 + B*4007	
B*0801 + B*40060101/40060102	B*0809 + B*4002	
B*0801 + B*4011	B*0812 + B*4002	
B*0801 + B*4018	B*0807 + B*4002	
B*0801 + B*4019	B*0804 + B*4013	
B*0801 + B*4020	B*0812 + B*4003	
B*0801 + B*4032	B*0807 + B*4016	
B*0801 + B*4033	B*0807 + B*400101/400102	B*0812 + B*4031
B*0801 + B*4037	B*0817 + B*4008	
B*0801 + B*4044	B*0809 + B*4018	B*0807 + B*40060101/40060102
B*0801 + B*4204	B*0809 + B*4201	
B*0801 + B*44G1	B*0802 + B*4409	
B*0801 + B*440301	B*0813 + B*44G1	
B*0801 + B*4803	B*0812 + B*4801	
B*0801 + B*4902	B*0802 + B*5001	
B*0801 + B*5107	B*0804 + B*51G1	
B*0801 + B*5109	B*0813 + B*5108	
B*0801 + B*5309	B*0802 + B*3520	
B*0801 + B*5503	B*0815 + B*5501	
B*0801 + B*5607	B*0802 + B*5601	
B*0802 + B*1806	B*0815 + B*1809	
B*0803 + B*51G1	B*0803 + B*5133	
B*0807 + B*3927	B*0815 + B*3915	
B*0807 + B*4011	B*0812 + B*4018	
B*0809 + B*1311	B*0812 + B*1302	
B*0809 + B*15010101/B*15010102N	B*0812 + B*1504	
B*0809 + B*390101/390103	B*0812 + B*390602	
B*0809 + B*4011	B*0812 + B*40060101/40060102	
B*0809 + B*5106	B*0812 + B*51G1	
B*0809 + B*5602	B*0812 + B*5601	
B*0809 + B*5610	B*0812 + B*5502	
B*1301 + B*1811	B*1306 + B*1810	
B*1301 + B*2715	B*1306 + B*2704	
B*1301 + B*3537	B*1302 + B*350101/3540N/3542	
B*1301 + B*4039	B*1306 + B*4002	
B*1301 + B*51G1	B*1302 + B*5104	
B*1301 + B*5106	B*1311 + B*5104	
B*1301 + B*5121	B*1306 + B*5116	
B*1302 + B*15010101/B*15010102N	B*1311 + B*1504	
B*1302 + B*1525	B*1309 + B*1536	
B*1302 + B*180101/1817N	B*1309 + B*1809	
B*1302 + B*3520	B*1309 + B*5309	
B*1302 + B*390101/390103	B*1311 + B*390602	
B*1302 + B*3905	B*1309 + B*380201	
B*1302 + B*4011	B*1311 + B*40060101/40060102	
B*1302 + B*4409	B*1309 + B*44G1	
B*1302 + B*5001	B*1309 + B*4902	
B*1302 + B*5106	B*1311 + B*51G1	
B*1302 + B*5601	B*1309 + B*5607	
B*1302 + B*5602	B*1311 + B*5601	
B*1302 + B*5610	B*1311 + B*5502	

B*1401 + B*270503	B*1402 + B*270503	
B*1401 + B*3805	B*1402 + B*3801	
B*1401 + B*3907	B*1402 + B*3907	
B*1401 + B*4405	B*1402 + B*4405	
B*1402 + B*1565	B*1403 + B*1539	
B*1402 + B*1813	B*1403 + B*180101/1817N	
B*1402 + B*3508	B*1403 + B*350101/3540N/3542	
B*1402 + B*3518	B*1403 + B*350902	
B*1402 + B*4428	B*1403 + B*440302	
B*1402 + B*5129	B*1403 + B*51G1	
B*1402 + B*5702	B*1403 + B*570301	
B*1405 + B*15010101/B*15010102N	B*140601 + B*1507	
B*1405 + B*1563	B*140601 + B*1545	
B*1405 + B*180101/1817N	B*140601 + B*1814	
B*1405 + B*350101/3540N/3542	B*140602 + B*3530	
B*1405 + B*390101/390103	B*140601 + B*3903	
B*1405 + B*4011	B*140601 + B*4002	
B*1405 + B*4020	B*140601 + B*4003	
B*1405 + B*4033	B*140601 + B*4031	
B*1405 + B*4803	B*140601 + B*4801	
B*140601 + B*390602	B*140602 + B*390601	
B*140601 + B*440302	B*140602 + B*440301	
B*15010101/B*15010102N + B*1502	B*1515 + B*1525	
B*15010101/B*15010102N + B*1503	B*1539 + B*1554	
B*15010101/B*15010102N + B*1508	B*1515 + B*1556	
B*15010101/B*15010102N + B*1510	B*1518 + B*1563	
B*15010101/B*15010102N + B*1513	B*1502 + B*1524	
B*15010101/B*15010102N + B*1518	B*1564 + B*1566	
B*15010101/B*15010102N + B*1521	B*1502 + B*1566	
B*15010101/B*15010102N + B*1523	B*1518 + B*1524	
B*15010101/B*15010102N + B*1529	B*1556 + B*1564 B*1503 + B*1508	
B*15010101/B*15010102N + B*1537	B*1510 + B*1538	
B*15010101/B*15010102N + B*1544	B*1521 + B*1550	
B*15010101/B*15010102N + B*1545	B*1507 + B*1563	
B*15010101/B*15010102N + B*1561	B*1503 + B*1570	
B*15010101/B*15010102N + B*1564	B*1503 + B*1515	
B*15010101/B*15010102N +	B*1515 + B*1812	B*1538 + B*1811
B*180101/1817N		
B*15010101/B*15010102N + B*1803	B*1570 + B*180101/1817N	
B*15010101/B*15010102N + B*1807	B*1556 + B*180101/1817N	B*1508 + B*1812
B*15010101/B*15010102N + B*1814	B*1507 + B*180101/1817N	
B*15010101/B*15010102N + B*1818	B*1532 + B*180101/1817N	
B*15010101/B*15010102N + B*2702	B*1524 + B*2708	
B*15010101/B*15010102N + B*2704	B*1540 + B*2725	
B*15010101/B*15010102N +	B*1543 + B*2708	
B*270502/270504/2713		
B*15010101/B*15010102N + B*270503	B*1571 + B*270503	B*1538 + B*270503
B*15010101/B*15010102N + B*2716	B*1543 + B*2712	
B*15010101/B*15010102N +	B*1520 + B*3543	B*1556 + B*3520
B*350101/3540N/3542		B*1508 + B*3528
B*15010101/B*15010102N + B*3503	B*1505 + B*3514	
B*15010101/B*15010102N + B*3504	B*1515 + B*3513	
B*15010101/B*15010102N + B*3506	B*1520 + B*3544	
B*15010101/B*15010102N + B*3511	B*1558 + B*350101/3540N/3542	
B*15010101/B*15010102N + B*3517	B*1539 + B*3514	
B*15010101/B*15010102N + B*3520	B*1515 + B*3516	
B*15010101/B*15010102N + B*3521	B*1515 + B*3528	
B*15010101/B*15010102N + B*3521	B*1538 + B*3511	
B*15010101/B*15010102N + B*3524	B*1538 + B*350101/3540N/3542	
B*15010101/B*15010102N + B*3529	B*1570 + B*350101/3540N/3542	
B*15010101/B*15010102N + B*3530	B*1534 + B*3517	
B*15010101/B*15010102N + B*3534	B*1563 + B*350101/3540N/3542	
B*15010101/B*15010102N + B*3545	B*1514 + B*3508	
B*15010101/B*15010102N + B*3704	B*1538 + B*3701	
B*15010101/B*15010102N + B*3801	B*1524 + B*3905	
B*15010101/B*15010102N +	B*1515 + B*3922	B*1570 + B*3905
B*390101/390103		
B*15010101/B*15010102N + B*390202	B*1570 + B*3913	
B*15010101/B*15010102N + B*3903	B*1507 + B*390101/390103	

B*15010101/B*15010102N + B*390602	B*1504 + B*390101/390103		
B*15010101/B*15010102N + B*3907	B*150104 + B*3907	B*1571 + B*3907	
B*15010101/B*15010102N + B*3909	B*1532 + B*390101/390103		
B*15010101/B*15010102N + B*3910	B*151101 + B*390202		
B*15010101/B*15010102N + B*3922	B*1566 + B*390201		
B*15010101/B*15010102N + B*400101/400102	B*1563 + B*4038		
B*15010101/B*15010102N + B*4002	B*1507 + B*4011		
B*15010101/B*15010102N + B*4003	B*1507 + B*4020		
B*15010101/B*15010102N + B*40060101/40060102	B*1504 + B*4011		
B*15010101/B*15010102N + B*4007	B*1556 + B*400101/400102		
B*15010101/B*15010102N + B*4008	B*1508 + B*4002		
B*15010101/B*15010102N + B*4013	B*1556 + B*4019		
B*15010101/B*15010102N + B*4018	B*1545 + B*4020	B*1563 + B*4003	
B*15010101/B*15010102N + B*4019	B*1524 + B*4002		
B*15010101/B*15010102N + B*4025	B*1515 + B*400101/400102		
B*15010101/B*15010102N + B*4031	B*1507 + B*4033		
B*15010101/B*15010102N + B*4043	B*1570 + B*400101/400102		
B*15010101/B*15010102N + B*44G1	B*1546 + B*4408		
B*15010101/B*15010102N + B*4405	B*1546 + B*4405	B*150104 + B*4405	B*1553 + B*4405
B*1571 + B*4405	B*1560 + B*4405		
B*15010101/B*15010102N + B*4412	B*1515 + B*44G1		
B*15010101/B*15010102N + B*4418	B*1524 + B*4501		
B*15010101/B*15010102N + B*4421	B*1514 + B*4416		
B*15010101/B*15010102N + B*4501	B*1514 + B*4504		
B*15010101/B*15010102N + B*47010101/47010102	B*1543 + B*4702		
B*15010101/B*15010102N + B*4801	B*1507 + B*4803	B*1568 + B*4021	
B*15010101/B*15010102N + B*4806	B*1508 + B*4801		
B*15010101/B*15010102N + B*4901	B*1524 + B*5001		
B*15010101/B*15010102N + B*5002	B*1514 + B*5001		
B*15010101/B*15010102N + B*51G1	B*3543 + B*5202	B*1556 + B*5107	B*1524 + B*780202
	B*1504 + B*5106	B*1508 + B*520102	B*1538 + B*51020
	B*150102 + B*510104		
B*15010101/B*15010102N + B*510102	B*1524 + B*780201	B*1508 + B*520101	B*1538 + B*510202
B*15010101/B*15010102N + B*5107	B*1515 + B*520102		
B*15010101/B*15010102N + B*511302	B*150102 + B*511301		
B*15010101/B*15010102N + B*5116	B*1538 + B*5134		
B*15010101/B*15010102N + B*5120	B*1570 + B*5108		
B*15010101/B*15010102N + B*5121	B*1550 + B*51G1		
B*15010101/B*15010102N + B*5122	B*1566 + B*5107		
B*15010101/B*15010102N + B*5123	B*1514 + B*510201		
B*15010101/B*15010102N + B*520101	B*1524 + B*7805		
B*15010101/B*15010102N + B*5301	B*1524 + B*350101/3540N/3542		
B*15010101/B*15010102N + B*5302	B*1538 + B*5301 + B*1524 + B*3524		
B*15010101/B*15010102N + B*5303	B*1543 + B*350101/3540N/3542		
B*15010101/B*15010102N + B*5304	B*1524 + B*3503		
B*15010101/B*15010102N + B*5308	B*1524 + B*3511		
B*15010101/B*15010102N + B*5402	B*1571 + B*5401		
B*15010101/B*15010102N + B*5502	B*1550 + B*5601	B*1504 + B*5610	
B*15010101/B*15010102N + B*5601	B*1504 + B*5602		
B*15010101/B*15010102N + B*5602	B*1534 + B*5604		
B*15010101/B*15010102N + B*5610	B*1550 + B*5602		
B*15010101/B*15010102N + B*5707	B*1514 + B*570301		
B*15010101/B*15010102N + B*5807	B*1514 + B*5802		
B*15010101/B*15010102N + B*7801	B*1570 + B*780202		
B*15010101/B*15010102N + B*780201	B*1508 + B*7805		
B*1502 + B*1503	B*1525 + B*1564		
B*1502 + B*1518	B*1521 + B*1564		
B*1502 + B*1523	B*1513 + B*1518		
B*1502 + B*1556	B*1508 + B*1525		
B*1502 + B*1812	B*1525 + B*180101/1817N		
B*1502 + B*2702	B*1513 + B*2708		
B*1502 + B*3505	B*1555 + B*3511		
B*1502 + B*3513	B*1525 + B*3503		
B*1502 + B*3516	B*1525 + B*3517		
B*1502 + B*3528	B*1525 + B*3520		
B*1502 + B*3801	B*1513 + B*3905		

B*1502 + B*3922	B*1521 + B*390201	B*1525 + B*390101/390103
B*1502 + B*400101/400102	B*1525 + B*4025	
B*1502 + B*4019	B*1513 + B*4002	
B*1502 + B*44G1	B*1525 + B*4412	
B*1502 + B*4418	B*1513 + B*4501	
B*1502 + B*4901	B*1513 + B*5001	
B*1502 + B*51G1	B*1513 + B*780202	
B*1502 + B*510102	B*1513 + B*780201	
B*1502 + B*5122	B*1521 + B*5107	
B*1502 + B*520101	B*1513 + B*7805	
B*1502 + B*520102	B*1525 + B*5107	
B*1502 + B*5301	B*1513 + B*350101/3540N/3542	
B*1502 + B*5302	B*1513 + B*3524	
B*1502 + B*5304	B*1513 + B*3503	
B*1502 + B*5308	B*1513 + B*3511	
B*1503 + B*1521	B*1518 + B*1525	
B*1503 + B*180101/1817N	B*1564 + B*1812	
B*1503 + B*1803	B*1561 + B*180101/1817N	
B*1503 + B*1807	B*1529 + B*1812	
B*1503 + B*350101/3540N/3542	B*1529 + B*3528	
B*1503 + B*3503	B*1564 + B*3513	
B*1503 + B*3514	B*1554 + B*3511	
B*1503 + B*3517	B*1564 + B*3516	
B*1503 + B*3520	B*1564 + B*3528	
B*1503 + B*3529	B*1561 + B*350101/3540N/3542	
B*1503 + B*3535	B*1569 + B*350101/3540N/3542	
B*1503 + B*390101/390103	B*1564 + B*3922	B*1561 + B*3905
B*1503 + B*390202	B*1561 + B*3913	B*1518 + B*390201
B*1503 + B*4008	B*1529 + B*4002	
B*1503 + B*4025	B*1564 + B*400101/400102	
B*1503 + B*4043	B*1561 + B*400101/400102	
B*1503 + B*4412	B*1564 + B*44G1	
B*1503 + B*4806	B*1529 + B*4801	
B*1503 + B*51G1	B*1529 + B*520102	
B*1503 + B*510102	B*1529 + B*520101	
B*1503 + B*5107	B*1564 + B*520102	
B*1503 + B*5120	B*1561 + B*5108	
B*1503 + B*5122	B*1518 + B*520102	
B*1503 + B*7801	B*1561 + B*780202	
B*1503 + B*780201	B*1529 + B*7805	
B*1504 + B*3505	B*1507 + B*3537	
B*1504 + B*3903	B*1507 + B*390602	
B*1504 + B*3909	B*1532 + B*390602	
B*1504 + B*4002	B*1507 + B*40060101/40060102	
B*1504 + B*4018	B*1507 + B*4044	
B*1504 + B*4201	B*1507 + B*4204	
B*1505 + B*1815	B*1539 + B*180101/1817N	
B*1505 + B*2710	B*1539 + B*270502/270504/2713	
B*1505 + B*3511	B*1539 + B*350101/3540N/3542	
B*1505 + B*3521	B*1539 + B*3524	
B*1505 + B*5101	B*1539 + B*5109	
B*1505 + B*5116	B*1540 + B*5109	B*1539 + B*5131
B*1505 + B*5129	B*1565 + B*5109	
B*1505 + B*5308	B*1539 + B*5301	
B*1505 + B*5501	B*1539 + B*5502	
B*1505 + B*5806	B*1539 + B*5802	
B*1507 + B*1510	B*1518 + B*1545	
B*1507 + B*1803	B*1570 + B*1814	
B*1507 + B*1807	B*1556 + B*1814	
B*1507 + B*1818	B*1532 + B*1814	
B*1507 + B*3534	B*1545 + B*350101/3540N/3542	
B*1507 + B*3909	B*1532 + B*3903	
B*1507 + B*400101/400102	B*1545 + B*4038	
B*1507 + B*4018	B*1545 + B*4003	
B*1507 + B*4802	B*1520 + B*1568	
B*1508 + B*1561	B*1529 + B*1570	
B*1508 + B*1564	B*1515 + B*1529	
B*1508 + B*180101/1817N	B*1515 + B*1807	
B*1508 + B*3513	B*1556 + B*3503	

B*1508 + B*3516	B*1556 + B*3517	
B*1508 + B*3520	B*1515 + B*350101/3540N/3542	
B*1508 + B*3922	B*1556 + B*390101/390103	
B*1508 + B*400101/400102	B*1556 + B*4025	B*1515 + B*4007
B*1508 + B*4019	B*1524 + B*4008	B*1515 + B*4013
B*1508 + B*44G1	B*1556 + B*4412	
B*1508 + B*4405	B*3543 + B*4405	
B*1508 + B*5107	B*1515 + B*51G1	
B*1510 + B*1524	B*1523 + B*1563	
B*1510 + B*180101/1817N	B*1537 + B*1811	
B*1510 + B*270503	B*1537 + B*270503	
B*1510 + B*350101/3540N/3542	B*1518 + B*3534	
B*1510 + B*3521	B*1537 + B*3511	
B*1510 + B*3524	B*1537 + B*350101/3540N/3542	
B*1510 + B*3704	B*1537 + B*3701	
B*1510 + B*4003	B*1518 + B*4018	
B*1510 + B*4038	B*1518 + B*400101/400102	
B*1510 + B*51G1	B*1537 + B*510201	
B*1510 + B*510102	B*1537 + B*510202	
B*1510 + B*5116	B*1537 + B*5134	
B*1510 + B*5301	B*1523 + B*5334	
B*1510 + B*5302	B*1537 + B*5301	
B*151101 + B*4405	B*151102 + B*4405	
B*1513 + B*1566	B*1521 + B*1524	
B*1513 + B*3505	B*1555 + B*5308	
B*1513 + B*3513	B*1525 + B*5304	
B*1514 + B*4901	B*1524 + B*5002	
B*1514 + B*51G1	B*1538 + B*5123	
B*1515 + B*1561	B*1564 + B*1570	
B*1515 + B*4043	B*1570 + B*4025	
B*1518 + B*1556	B*1529 + B*1566	
B*1518 + B*2702	B*1523 + B*2708	
B*1518 + B*350901	B*1572 + B*3504	
B*1518 + B*3515	B*1552 + B*3511	
B*1518 + B*3801	B*1523 + B*3905	
B*1518 + B*4002	B*1552 + B*4005	B*1572 + B*4035
B*1518 + B*4019	B*1523 + B*4002	
B*1518 + B*4418	B*1523 + B*4501	
B*1518 + B*4501	B*1551 + B*5002	
B*1518 + B*4504	B*1551 + B*5001	
B*1518 + B*4901	B*1523 + B*5001	
B*1518 + B*51G1	B*1523 + B*780202	B*1529 + B*5122
B*1518 + B*510102	B*1523 + B*780201	
B*1518 + B*5107	B*1564 + B*5122	
B*1518 + B*5108	B*1551 + B*51G1	
B*1518 + B*5124	B*1572 + B*510104	
B*1518 + B*5131	B*1552 + B*51G1	
B*1518 + B*520101	B*1523 + B*7805	
B*1518 + B*5301	B*1523 + B*350101/3540N/3542	
B*1518 + B*5302	B*1523 + B*3524	
B*1518 + B*5304	B*1523 + B*3503	
B*1518 + B*5308	B*1523 + B*3511	
B*1518 + B*7801	B*1529 + B*7803	
B*1520 + B*1529	B*1539 + B*5525	
B*1520 + B*4405	B*3528 + B*4405	
B*1520 + B*4803	B*4021 + B*4802	
B*1520 + B*51G1	B*350101/3540N/3542 + B*5202	
B*1520 + B*5107	B*3520 + B*5202	
B*1520 + B*5116	B*3515 + B*5202	
B*1520 + B*5129	B*3508 + B*5202	
B*1520 + B*520102	B*3528 + B*5202	
B*1520 + B*5501	B*1542 + B*5609	
B*1521 + B*5121	B*1544 + B*51G1	
B*1521 + B*520102	B*1525 + B*5122	
B*1521 + B*5502	B*1544 + B*5601	
B*1521 + B*5610	B*1544 + B*5602	
B*1523 + B*3515	B*1552 + B*5308	
B*1523 + B*390201	B*1561 + B*3801	
B*1523 + B*4504	B*1551 + B*4901	

B*1524 + B*270502/270504/2713	B*1543 + B*2702
B*1524 + B*3506	B*1558 + B*5301
B*1524 + B*3521	B*1538 + B*5308
B*1524 + B*3529	B*1570 + B*5301
B*1524 + B*3534	B*1563 + B*5301
B*1524 + B*390101/390103	B*1570 + B*3801
B*1524 + B*5303	B*1543 + B*5301
B*1524 + B*7801	B*1570 + B*51G1
B*1524 + B*7803	B*1570 + B*5122
B*1525 + B*1809	B*1536 + B*180101/1817N
B*1525 + B*380201	B*1536 + B*3905
B*1525 + B*44G1	B*1536 + B*4409
B*1525 + B*4902	B*1536 + B*5001
B*1525 + B*5309	B*1536 + B*3520
B*1525 + B*5607	B*1536 + B*5601
B*1527 + B*51G1	B*1527 + B*5133
B*1529 + B*180101/1817N	B*1564 + B*1807
B*1529 + B*3520	B*1564 + B*350101/3540N/3542
B*1529 + B*400101/400102	B*1564 + B*4007
B*1529 + B*4019	B*1564 + B*4013
B*1529 + B*5107	B*1564 + B*51G1
B*1530 + B*51G1	B*1530 + B*5133
B*1531 + B*51G1	B*1531 + B*5133
B*1532 + B*1803	B*1570 + B*1818
B*1532 + B*1807	B*1556 + B*1818
B*1538 + B*3506	B*1558 + B*3524
B*1538 + B*3529	B*1570 + B*3524
B*1538 + B*3534	B*1563 + B*3524
B*1538 + B*5303	B*1543 + B*3524
B*1539 + B*1813	B*1565 + B*180101/1817N
B*1539 + B*3508	B*1565 + B*350101/3540N/3542
B*1539 + B*3515	B*1540 + B*350101/3540N/3542
B*1539 + B*3518	B*1565 + B*350902
B*1539 + B*3533	B*1540 + B*3503
B*1539 + B*4421	B*1540 + B*44G1
B*1539 + B*4428	B*1565 + B*440302
B*1539 + B*5116	B*1540 + B*51G1
B*1539 + B*5129	B*1565 + B*51G1
B*1539 + B*5134	B*1540 + B*51Q201
B*1539 + B*5702	B*1565 + B*570301
B*1540 + B*3508	B*1565 + B*3515
B*1540 + B*5129	B*1565 + B*5116
B*1543 + B*3506	B*1558 + B*5303
B*1543 + B*3529	B*1570 + B*5303
B*1543 + B*3534	B*1563 + B*5303
B*1545 + B*180101/1817N	B*1563 + B*1814
B*1545 + B*390101/390103	B*1563 + B*3903
B*1545 + B*4011	B*1563 + B*4002
B*1545 + B*4033	B*1563 + B*4031
B*1545 + B*4036	B*1558 + B*4031
B*1545 + B*4803	B*1563 + B*4801
B*1546 + B*3907	B*1553 + B*3907
B*1551 + B*3535	B*1552 + B*3538
B*1551 + B*5131	B*1552 + B*5108
B*1556 + B*1803	B*1570 + B*1807
B*1556 + B*4043	B*1570 + B*4007
B*1556 + B*5122	B*1566 + B*51G1
B*1556 + B*7803	B*1566 + B*7801
B*1558 + B*3529	B*1570 + B*3506
B*1558 + B*3534	B*1563 + B*3506
B*1558 + B*4033	B*1563 + B*4036
B*1558 + B*4501	B*1573 + B*4502
B*1561 + B*3535	B*1569 + B*3529
B*1561 + B*4025	B*1564 + B*4043
B*1563 + B*3529	B*1570 + B*3534
B*180101/1817N + B*270503	B*1804 + B*270503
B*180101/1817N + B*2706	B*1802 + B*2721
B*180101/1817N + B*2710	B*1815 + B*270502/270504/2713
B*180101/1817N +	B*1811 + B*3524 B*1807 + B*3520

B*1811 + B*270503

B*350101/3540N/3542

B*180101/1817N + B*3508	B*1813 + B*350101/3540N/3542	
B*180101/1817N + B*3511	B*1811 + B*3521	B*1815 + B*350101/3540N/3542
B*180101/1817N + B*3513	B*1812 + B*3503	
B*180101/1817N + B*3516	B*1812 + B*3517	
B*180101/1817N + B*3518	B*1813 + B*350902	
B*180101/1817N + B*3521	B*1815 + B*3524	
B*180101/1817N + B*3528	B*1812 + B*3520	
B*180101/1817N + B*3529	B*1803 + B*350101/3540N/3542	
B*180101/1817N + B*3701	B*1811 + B*3704	
B*180101/1817N + B*380201	B*1809 + B*3905	
B*180101/1817N + B*390101/390103	B*1803 + B*3905	
B*180101/1817N + B*390202	B*1803 + B*3913	
B*180101/1817N + B*3903	B*1814 + B*390101/390103	
B*180101/1817N + B*3907	B*1804 + B*3907	
B*180101/1817N + B*3909	B*1818 + B*390101/390103	
B*180101/1817N + B*3922	B*1812 + B*390101/390103	
B*180101/1817N + B*3927	B*1806 + B*390101/390103	
B*180101/1817N + B*400101/400102	B*1812 + B*4025	
B*180101/1817N + B*4002	B*1814 + B*4011	
B*180101/1817N + B*4003	B*1814 + B*4020	
B*180101/1817N + B*4007	B*1807 + B*400101/400102	
B*180101/1817N + B*4013	B*1807 + B*4019	
B*180101/1817N + B*4031	B*1814 + B*4033	
B*180101/1817N + B*4043	B*1803 + B*400101/400102	
B*180101/1817N + B*44G1	B*1812 + B*4412 B*1809 + B*4409	
B*180101/1817N + B*4405	B*1804 + B*4405	
B*180101/1817N + B*4428	B*1813 + B*440302	
B*180101/1817N + B*4801	B*1814 + B*4803	
B*180101/1817N + B*4902	B*1809 + B*5001	
B*180101/1817N + B*51G1	B*1815 + B*5109 B*1807 + B*5107	
B*180101/1817N + B*510201	B*1811 + B*51G1	
B*180101/1817N + B*510202	B*1811 + B*510102	
B*180101/1817N + B*5116	B*1815 + B*5131	
B*180101/1817N + B*5120	B*1803 + B*5108	
B*180101/1817N + B*5129	B*1813 + B*51G1	
B*180101/1817N + B*5134	B*1811 + B*5116	B*1810 + B*5121
B*180101/1817N + B*520102	B*1812 + B*5107	
B*180101/1817N + B*5301	B*1811 + B*5302	
B*180101/1817N + B*5308	B*1815 + B*5301	
B*180101/1817N + B*5309	B*1809 + B*3520	
B*180101/1817N + B*5501	B*1815 + B*5502	
B*180101/1817N + B*5503	B*1806 + B*5501	
B*180101/1817N + B*5607	B*1809 + B*5601	
B*180101/1817N + B*5702	B*1813 + B*570301	
B*180101/1817N + B*5806	B*1815 + B*5802	
B*180101/1817N + B*7801	B*1803 + B*780202	
B*1803 + B*2701	B*1809 + B*2708	
B*1803 + B*3508	B*1813 + B*3529	
B*1803 + B*3511	B*1815 + B*3529	
B*1803 + B*380201	B*1809 + B*390101/390103	
B*1803 + B*3908	B*1813 + B*390201	
B*1803 + B*4007	B*1807 + B*4043	
B*1806 + B*3903	B*1814 + B*3927	
B*1806 + B*3909	B*1818 + B*3927	
B*1806 + B*3922	B*1812 + B*3927	
B*1807 + B*3528	B*1812 + B*350101/3540N/3542	
B*1807 + B*4002	B*1812 + B*4008	
B*1807 + B*4801	B*1812 + B*4806	
B*1807 + B*520101	B*1812 + B*510102	
B*1807 + B*520102	B*1812 + B*51G1	
B*1807 + B*5309	B*1809 + B*350101/3540N/3542	
B*1807 + B*7805	B*1812 + B*780201	
B*1809 + B*3528	B*1812 + B*5309	
B*1810 + B*2715	B*1811 + B*2704	
B*1810 + B*4039	B*1811 + B*4002	
B*1811 + B*5129	B*1813 + B*510201	
B*1811 + B*520102	B*1815 + B*5203	

B*1811 + B*780201	B*1815 + B*7804
B*1812 + B*3903	B*1814 + B*3922
B*1812 + B*3909	B*1818 + B*3922
B*1813 + B*3511	B*1815 + B*3508
B*1813 + B*510202	B*1815 + B*5105
B*1814 + B*3909	B*1818 + B*3903
B*2701 + B*390101/390103	B*2708 + B*380201
B*2702 + B*350101/3540N/3542	B*2708 + B*5301
B*2702 + B*3503	B*2708 + B*5304
B*2702 + B*3511	B*2708 + B*5308
B*2702 + B*3524	B*2708 + B*5302
B*2702 + B*3905	B*2708 + B*3801
B*2702 + B*4002	B*2708 + B*4019
B*2702 + B*4501	B*2708 + B*4418
B*2702 + B*5001	B*2708 + B*4901
B*2702 + B*5303	B*270502/270504/2713 + B*5301
B*2702 + B*780201	B*2708 + B*510102
B*2702 + B*780202	B*2708 + B*51G1
B*2702 + B*7805	B*2708 + B*520101
B*2704 + B*2707	B*2710 + B*2711
B*2704 + B*4039	B*2715 + B*4002
B*2704 + B*5121	B*2715 + B*5116
B*270502/270504/2713 + B*270503	B*270503 + B*270506
B*270502/270504/2713 + B*2712	B*2708 + B*2716
B*270502/270504/2713 +	B*2708 + B*5303
B*350101/3540N/3542	
B*270502/270504/2713 + B*3511	B*2710 + B*350101/3540N/3542
B*270502/270504/2713 + B*3521	B*2710 + B*3524
B*270502/270504/2713 + B*3907	B*270506 + B*3907
B*270502/270504/2713 + B*4405	B*270506 + B*4405
B*270502/270504/2713 + B*4702	B*2708 + B*47010101/47010102
B*270502/270504/2713 + B*51G1	B*2710 + B*5109
B*270502/270504/2713 + B*5116	B*2710 + B*5131
B*270502/270504/2713 + B*5308	B*2710 + B*5301
B*270502/270504/2713 + B*5501	B*2710 + B*5502
B*270502/270504/2713 + B*5806	B*2710 + B*5802
B*270503 + B*350101/3540N/3542	B*270503 + B*5307
B*270503 + B*3511	B*270503 + B*3521
B*270503 + B*3701	B*270503 + B*3704
B*270503 + B*3801	B*270503 + B*3805
B*270503 + B*390101/390103	B*270503 + B*3904
B*270503 + B*4002	B*270503 + B*4040
B*270503 + B*4101	B*270503 + B*4106
B*270503 + B*4201	B*270503 + B*4202
B*270503 + B*44G1	B*270503 + B*4422
B*270503 + B*4801	B*270503 + B*4804
B*270503 + B*51G1	B*270503 + B*510201
B*270503 + B*510102	B*270503 + B*510202
B*270503 + B*5116	B*270503 + B*5133
B*270503 + B*520101	
B*270503 + B*5301	B*270503 + B*520102
B*270503 + B*5306	B*270503 + B*5308
B*270503 + B*5401	B*270503 + B*5402
B*270503 + B*5502	B*270503 + B*5510
B*270503 + B*780201	B*270503 + B*780202
B*2712 + B*47010101/47010102	B*2716 + B*4702
B*2712 + B*5303	B*2716 + B*350101/3540N/3542
B*350101/3540N/3542 + B*3518	B*3508 + B*350902
B*350101/3540N/3542 + B*3521	B*3511 + B*3524
B*350101/3540N/3542 + B*3533	B*3503 + B*3515
B*350101/3540N/3542 + B*3544	B*3504 + B*3543
B*350101/3540N/3542 + B*3704	B*3524 + B*3701
B*350101/3540N/3542 + B*3801	B*3905 + B*5301
B*350101/3540N/3542 +	B*3529 + B*3905
B*390101/390103	
B*350101/3540N/3542 + B*390202	B*3529 + B*3913
B*350101/3540N/3542 + B*3907	B*3507 + B*3907
B*350101/3540N/3542 +	B*3520 + B*4007
B*400101/400102	B*3534 + B*4038

B*350101/3540N/3542 + B*4002	B*3528 + B*4008	B*3504 + B*4003	
B*350101/3540N/3542 + B*4011	B*3504 + B*4020	B*3532 + B*4004	
B*350101/3540N/3542 + B*4018	B*3534 + B*4003		
B*350101/3540N/3542 + B*4019	B*3520 + B*4013	B*4002 + B*5301	B*4037 + B*5305
B*350101/3540N/3542 + B*4036	B*3503 + B*4038		
B*350101/3540N/3542 + B*4037	B*3527 + B*4002		
B*350101/3540N/3542 + B*4043	B*3529 + B*400101/400102		
B*350101/3540N/3542 + B*4405	B*3507 + B*4405	B*3519 + B*4405	
B*350101/3540N/3542 + B*4418	B*4501 + B*5301		
B*350101/3540N/3542 + B*4421	B*3515 + B*44G1		
B*350101/3540N/3542 + B*4428	B*3508 + B*440302		
B*350101/3540N/3542 + B*47010101/47010102	B*4702 + B*5303		
B*350101/3540N/3542 + B*4801	B*3528 + B*4806		
B*350101/3540N/3542 + B*4901	B*5001 + B*5301		
B*350101/3540N/3542 + B*51G1	B*5306 + B*7804	B*3537 + B*5104	B*5301 + B*780202
B*3511 + B*5109	B*3524 + B*510201		
B*350101/3540N/3542 + B*510102	B*5301 + B*780201	B*3524 + B*510202	
B*350101/3540N/3542 + B*510202	B*5308 + B*7804		
B*350101/3540N/3542 + B*5107	B*3520 + B*51G1		
B*350101/3540N/3542 + B*5116	B*3515 + B*51G1	B*3524 + B*5134	B*3511 + B*5131
B*350101/3540N/3542 + B*5120	B*3529 + B*5108		
B*350101/3540N/3542 + B*5129	B*3508 + B*51G1		
B*350101/3540N/3542 + B*5131	B*3515 + B*5109		
B*350101/3540N/3542 + B*5134	B*3515 + B*510201		
B*350101/3540N/3542 + B*520101	B*5301 + B*7805	B*3528 + B*510102	
B*350101/3540N/3542 + B*520102	B*3528 + B*51G1	B*3521 + B*5203	
B*350101/3540N/3542 + B*5301	B*3527 + B*5305		
B*350101/3540N/3542 + B*5302	B*3524 + B*5301		
B*350101/3540N/3542 + B*5304	B*3503 + B*5301		
B*350101/3540N/3542 + B*5308	B*3511 + B*5301		
B*350101/3540N/3542 + B*5501	B*3511 + B*5502		
B*350101/3540N/3542 + B*5512	B*3527 + B*5502		
B*350101/3540N/3542 + B*5605	B*5609 + B*780202		
B*350101/3540N/3542 + B*5611	B*3503 + B*5609		
B*350101/3540N/3542 + B*5702	B*3508 + B*570301		
B*350101/3540N/3542 + B*570301	B*3504 + B*570101		
B*350101/3540N/3542 + B*5806	B*3511 + B*5802		
B*350101/3540N/3542 + B*7801	B*3529 + B*780202		
B*350101/3540N/3542 + B*780201	B*3521 + B*7804		
B*350101/3540N/3542 + B*7805	B*3528 + B*780201		
B*3503 + B*3504	B*3506 + B*3534		
B*3503 + B*3512	B*3506 + B*3539		
B*3503 + B*3516	B*3513 + B*3517		
B*3503 + B*3528	B*3513 + B*3520		
B*3503 + B*3801	B*3905 + B*5304		
B*3503 + B*390101/390103	B*3506 + B*3915		
B*3503 + B*3914	B*3534 + B*3903		
B*3503 + B*3922	B*3513 + B*390101/390103		
B*3503 + B*400101/400102	B*3513 + B*4025	B*3506 + B*4033	B*3534 + B*4036
B*3503 + B*4002	B*3506 + B*4018		
B*3503 + B*40060101/40060102	B*3506 + B*4044		
B*3503 + B*4016	B*3506 + B*4032		
B*3503 + B*4019	B*4002 + B*5304		
B*3503 + B*44G1	B*3513 + B*4412	B*3538 + B*440301	
B*3503 + B*4418	B*4501 + B*5304		
B*3503 + B*4421	B*3533 + B*44G1		
B*3503 + B*4801	B*3534 + B*4807		
B*3503 + B*4901	B*5001 + B*5304		
B*3503 + B*51G1	B*5304 + B*780202	B*3534 + B*511302	
B*3503 + B*510102	B*5304 + B*780201		
B*3503 + B*510104	B*3534 + B*511301		
B*3503 + B*5108	B*3538 + B*5109		
B*3503 + B*5116	B*3533 + B*51G1		
B*3503 + B*5131	B*3533 + B*5109		
B*3503 + B*5134	B*3533 + B*510201		
B*3503 + B*520101	B*5304 + B*7805		
B*3503 + B*520102	B*3513 + B*5107		
B*3503 + B*5302	B*3524 + B*5304		

B*3503 + B*5308	B*3511 + B*5304	
B*3503 + B*5605	B*5611 + B*780202	
B*3504 + B*3539	B*3512 + B*3534	
B*3504 + B*3903	B*3506 + B*3914	
B*3504 + B*3915	B*3534 + B*390101/390103	
B*3504 + B*4002	B*350901 + B*4035	
B*3504 + B*4018	B*3534 + B*4002	
B*3504 + B*4032	B*3534 + B*4016	
B*3504 + B*4033	B*3534 + B*400101/400102	
B*3504 + B*4036	B*3506 + B*400101/400102	
B*3504 + B*4044	B*3534 + B*40060101/40060102	
B*3504 + B*4807	B*3506 + B*4801	
B*3504 + B*511301	B*3506 + B*510104	
B*3504 + B*511302	B*3506 + B*51G1	
B*3504 + B*5124	B*350901 + B*510104	
B*3505 + B*390602	B*3537 + B*3903	
B*3505 + B*40060101/40060102	B*3537 + B*4002	
B*3505 + B*4044	B*3537 + B*4018	
B*3505 + B*4204	B*3537 + B*4201	
B*3506 + B*5124	B*350901 + B*511301	
B*3508 + B*390201	B*3529 + B*3908	
B*3508 + B*4421	B*3545 + B*4416	
B*3508 + B*4501	B*3545 + B*4504	
B*3508 + B*5002	B*3545 + B*5001	
B*3508 + B*510102	B*3521 + B*5105	
B*3508 + B*510202	B*3511 + B*5105	
B*3508 + B*5107	B*3520 + B*5129	
B*3508 + B*5116	B*3515 + B*5129	
B*3508 + B*5123	B*3545 + B*510201	
B*3508 + B*520102	B*3528 + B*5129	
B*3508 + B*5707	B*3545 + B*570301	
B*3508 + B*5807	B*3545 + B*5802	
B*350902 + B*4428	B*3518 + B*440302	
B*350902 + B*5129	B*3518 + B*51G1	
B*350902 + B*5702	B*3518 + B*570301	
B*3510 + B*4101	B*3510 + B*4106	
B*3510 + B*4801	B*3510 + B*4804	
B*3511 + B*3704	B*3521 + B*3701	
B*3511 + B*3801	B*3905 + B*5308	
B*3511 + B*4002	B*3515 + B*4005	
B*3511 + B*4019	B*4002 + B*5308	
B*3511 + B*4418	B*4501 + B*5308	
B*3511 + B*4901	B*5001 + B*5308	
B*3511 + B*51G1	B*3521 + B*510201	B*5308 + B*780202
B*3511 + B*510102	B*3521 + B*510202	B*5308 + B*780201
B*3511 + B*5116	B*3521 + B*5134	
B*3511 + B*520101	B*5308 + B*7805	
B*3511 + B*5203	B*3528 + B*510201	
B*3511 + B*5302	B*3521 + B*5301	
B*3511 + B*5512	B*3527 + B*5501	B*3524 + B*5308
B*3512 + B*3915	B*3539 + B*390101/390103	
B*3512 + B*4018	B*3539 + B*4002	
B*3512 + B*4032	B*3539 + B*4016	
B*3512 + B*4033	B*3539 + B*400101/400102	
B*3512 + B*4044	B*3539 + B*40060101/40060102	
B*3515 + B*4036	B*3533 + B*4038	
B*3515 + B*5107	B*3520 + B*5116	
B*3515 + B*520102	B*3528 + B*5116	
B*3515 + B*5304	B*3533 + B*5301	
B*3515 + B*5611	B*3533 + B*5609	
B*3516 + B*3520	B*3517 + B*3528	
B*3516 + B*390101/390103	B*3517 + B*3922	
B*3516 + B*4025	B*3517 + B*400101/400102	
B*3516 + B*4412	B*3517 + B*44G1	
B*3516 + B*5107	B*3517 + B*520102	
B*3517 + B*5602	B*3530 + B*5604	
B*3520 + B*380201	B*3905 + B*5309	
B*3520 + B*3922	B*3528 + B*390101/390103	
B*3520 + B*400101/400102	B*3528 + B*4025	

B*3520 + B*44G1	B*4409 + B*5309	B*3528 + B*4412
B*3520 + B*4902	B*5001 + B*5309	
B*3520 + B*520102	B*3528 + B*5107	
B*3520 + B*5607	B*5309 + B*5601	
B*3521 + B*51G1	B*5306 + B*780201	
B*3521 + B*5109	B*3524 + B*51G1	B*5302 + B*780202
B*3521 + B*5131	B*3524 + B*5116	
B*3521 + B*520102	B*5306 + B*7805	
B*3521 + B*5502	B*3524 + B*5501	
B*3521 + B*5802	B*3524 + B*5806	
B*3522 + B*3918	B*3544 + B*3903	
B*3524 + B*3801	B*3905 + B*5302	
B*3524 + B*4019	B*4002 + B*5302	
B*3524 + B*4418	B*4501 + B*5302	
B*3524 + B*4901	B*5001 + B*5302	
B*3524 + B*510102	B*5302 + B*780201	
B*3524 + B*520101	B*5302 + B*7805	
B*3524 + B*5203	B*3528 + B*5109	
B*3527 + B*3910	B*3529 + B*3920	
B*3527 + B*4019	B*4037 + B*5301	
B*3529 + B*3801	B*390101/390103 + B*5301	
B*3529 + B*51G1	B*5301 + B*7801	
B*3529 + B*5122	B*5301 + B*7803	
B*3529 + B*5605	B*5609 + B*7801	
B*3531 + B*4405	B*4008 + B*4405	
B*3532 + B*5601	B*3537 + B*5604	
B*3533 + B*5108	B*3538 + B*5131	
B*3543 + B*4002	B*3544 + B*4003	
B*3543 + B*4011	B*3544 + B*4020	
B*3543 + B*570301	B*3544 + B*570101	
B*3701 + B*51G1	B*3704 + B*510201	
B*3701 + B*510102	B*3704 + B*510202	
B*3701 + B*5116	B*3704 + B*5134	
B*3701 + B*5302	B*3704 + B*5301	
B*3801 + B*3907	B*3805 + B*3907	
B*3801 + B*4002	B*3905 + B*4019	
B*3801 + B*4405	B*3805 + B*4405	
B*3801 + B*4501	B*3905 + B*4418	
B*3801 + B*4902	B*380201 + B*4901	
B*3801 + B*5001	B*3905 + B*4901	
B*3801 + B*5606	B*5122 + B*670101	
B*3801 + B*7801	B*390101/390103 + B*51G1	B*390602 + B*5106
B*3801 + B*780201	B*3905 + B*510102	
B*3801 + B*780202	B*3905 + B*51G1	
B*3801 + B*7803	B*390101/390103 + B*5122	
B*3801 + B*7805	B*3905 + B*520101	
B*380201 + B*4409	B*3905 + B*44G1	
B*380201 + B*5001	B*3905 + B*4902	
B*380201 + B*5601	B*3905 + B*5607	
B*3803 + B*4501	B*390201 + B*4415	
B*3806 + B*7803	B*3919 + B*51G1	
B*390101/390103 + B*3907	B*3907 + B*3912	B*3904 + B*3907
B*390101/390103 + B*3913	B*390202 + B*3905	
B*390101/390103 + B*400101/400102	B*3922 + B*4025	B*3905 + B*4043
B*390101/390103 + B*4002	B*3903 + B*4011	
B*390101/390103 + B*4003	B*3903 + B*4020	
B*390101/390103 + B*4004	B*390602 + B*4011	
B*40060101/40060102		
B*390101/390103 + B*4018	B*3915 + B*4002	
B*390101/390103 + B*4031	B*3903 + B*4033	
B*390101/390103 + B*4032	B*3915 + B*4016	
B*390101/390103 + B*4033	B*3915 + B*400101/400102	
B*390101/390103 + B*4044	B*3915 + B*40060101/40060102	
B*390101/390103 + B*44G1	B*3922 + B*4412	
B*390101/390103 + B*4405	B*3912 + B*4405	B*3904 + B*4405
B*390101/390103 + B*4801	B*3903 + B*4803	
B*390101/390103 + B*5108	B*3905 + B*5120	
B*390101/390103 + B*520102	B*3922 + B*5107	
B*390101/390103 + B*5502	B*390602 + B*5610	B*390201 + B*5122

B*390101/390103 + B*5503	B*3927 + B*5501		
B*390101/390103 + B*5601	B*390602 + B*5602		
B*390101/390103 + B*5606	B*670101 + B*7803		
B*390101/390103 + B*780202	B*3905 + B*7801		
B*390202 + B*400101/400102	B*3913 + B*4043		
B*390202 + B*5108	B*3913 + B*5120		
B*390202 + B*780202	B*3913 + B*7801		
B*3903 + B*400101/400102	B*3914 + B*4036		
B*3903 + B*40060101/40060102	B*390602 + B*4002		
B*3903 + B*4044	B*390602 + B*4018		
B*3903 + B*4204	B*390602 + B*4201		
B*3903 + B*4801	B*3914 + B*4807		
B*3903 + B*51G1	B*3914 + B*511302		
B*3903 + B*510104	B*3914 + B*511301		
B*390601 + B*440302	B*390602 + B*440301		
B*3907 + B*400101/400102	B*3907 + B*4010		
B*3907 + B*4002	B*3907 + B*4040		
B*3907 + B*4101	B*3907 + B*4106		
B*3907 + B*4201	B*3907 + B*4202		
B*3907 + B*44G1	B*3907 + B*4422		
B*3907 + B*440301	B*3907 + B*4426		
B*3907 + B*4801	B*3907 + B*4804		
B*3907 + B*51G1	B*3907 + B*5133	B*3907 + B*510102	
B*3907 + B*510201	B*3907 + B*510202		
B*3907 + B*520101	B*3907 + B*520102	B*3907 + B*5205	
B*3907 + B*5401	B*3907 + B*5402		
B*3907 + B*5502	B*3907 + B*5510		
B*3907 + B*780201	B*3907 + B*780202		
B*3911 + B*51G1	B*3911 + B*5133		
B*400101/400102 + B*4003	B*4018 + B*4038		
B*400101/400102 + B*4009	B*4002 + B*4042		
B*400101/400102 + B*4013	B*4007 + B*4019		
B*400101/400102 + B*4018	B*4002 + B*4033	B*4011 + B*4031	
B*400101/400102 + B*4032	B*4016 + B*4033		
B*400101/400102 + B*4044	B*40060101/40060102 + B*4033		
B*400101/400102 + B*44G1	B*4042 + B*4414		
B*400101/400102 + B*4405	B*4021 + B*4405	B*4010 + B*4405	
B*400101/400102 + B*4412	B*4025 + B*44G1		
B*400101/400102 + B*4807	B*4036 + B*4801		
B*400101/400102 + B*51G1	B*4007 + B*5107		
B*400101/400102 + B*510103	B*400103 + B*51G1		
B*400101/400102 + B*5107	B*4025 + B*520102		
B*400101/400102 + B*511301	B*4036 + B*510104		
B*400101/400102 + B*511302	B*4036 + B*51G1		
B*400101/400102 + B*5120	B*4043 + B*5108		
B*400101/400102 + B*7801	B*4043 + B*780202		
B*400103 + B*4405	B*4405 + B*4803		
B*400103 + B*511302	B*4036 + B*510103		
B*4002 + B*4020	B*4003 + B*4011		
B*4002 + B*4032	B*4016 + B*4018		
B*4002 + B*4044	B*40060101/40060102 + B*4018		
B*4002 + B*4104	B*4024 + B*4102		
B*4002 + B*4201	B*4040 + B*4202		
B*4002 + B*4204	B*40060101/40060102 + B*4201		
B*4002 + B*44G1	B*4009 + B*4414		
B*4002 + B*4405	B*4040 + B*4405		
B*4002 + B*4418	B*4019 + B*4501		
B*4002 + B*4432	B*4029 + B*440301		
B*4002 + B*4803	B*4011 + B*4801		
B*4002 + B*4806	B*4008 + B*4801		
B*4002 + B*4901	B*4019 + B*5001		
B*4002 + B*51G1	B*4005 + B*5131	B*4019 + B*780202	B*4008 + B*520102
B*4002 + B*510102	B*4019 + B*780201	B*4008 + B*520101	
B*4002 + B*510104	B*4035 + B*5124		
B*4002 + B*5121	B*4039 + B*5116		
B*4002 + B*520101	B*4019 + B*7805		
B*4002 + B*5512	B*4037 + B*5502		
B*4002 + B*570101	B*4003 + B*570301		
B*4002 + B*780201	B*4008 + B*7805		

B*4003 + B*4033	B*4020 + B*4031		
B*4003 + B*4803	B*4020 + B*4801		
B*40060101/40060102 + B*4032	B*4016 + B*4044		
B*40060101/40060102 + B*5106	B*4011 + B*51G1		
B*40060101/40060102 + B*5602	B*4011 + B*5601		
B*40060101/40060102 + B*5610	B*4011 + B*5502		
B*4008 + B*4803	B*4011 + B*4806		
B*4009 + B*4033	B*4018 + B*4042		
B*4011 + B*570101	B*4020 + B*570301		
B*4013 + B*5107	B*4019 + B*51G1		
B*4018 + B*4204	B*4044 + B*4201		
B*4031 + B*4803	B*4033 + B*4801		
B*4036 + B*5301	B*4038 + B*5304		
B*4036 + B*5609	B*4038 + B*5611		
B*4201 + B*4405	B*4202 + B*4405		
B*44G1 + B*4405	B*4405 + B*4408	B*4405 + B*4422	
B*44G1 + B*5001	B*4409 + B*4902		
B*44G1 + B*5107	B*4412 + B*520102		
B*44G1 + B*5109	B*440301 + B*5108		
B*44G1 + B*5116	B*4421 + B*51G1		
B*44G1 + B*5119	B*4429 + B*5108		
B*44G1 + B*5131	B*4421 + B*5109		
B*44G1 + B*5134	B*4421 + B*510201	B*4416 + B*5123	
B*44G1 + B*5601	B*4409 + B*5607		
B*440301 + B*4405	B*4405 + B*4426		
B*440301 + B*5119	B*4429 + B*5109		
B*440302 + B*4405	B*4405 + B*4407		
B*440302 + B*5129	B*4428 + B*51G1		
B*440302 + B*5702	B*4428 + B*570301		
B*4405 + B*4901	B*4405 + B*4903		
B*4405 + B*51G1	B*4405 + B*510102	B*4405 + B*5126	B*4405 + B*5133
B*4405 + B*510201	B*4405 + B*510202		
B*4405 + B*520101	B*4405 + B*5202	B*4405 + B*5204	B*4405 + B*5205
B*4405 + B*520102	B*4405 + B*520103		
B*4405 + B*5401	B*4405 + B*5402		
B*4405 + B*5502	B*4405 + B*5507	B*4405 + B*5510	
B*4405 + B*780201	B*4405 + B*780202		
B*4416 + B*4501	B*4421 + B*4504		
B*4416 + B*5002	B*4421 + B*5001		
B*4416 + B*5707	B*4421 + B*570301		
B*4416 + B*5807	B*4421 + B*5802		
B*4418 + B*5001	B*4501 + B*4901		
B*4418 + B*5606	B*4506 + B*5107		
B*4418 + B*7801	B*5002 + B*5120		
B*4418 + B*780201	B*4501 + B*510102		
B*4418 + B*780202	B*4501 + B*51G1	B*5002 + B*5108	
B*4418 + B*7805	B*4501 + B*520101		
B*4501 + B*5001	B*4504 + B*5002		
B*4501 + B*510201	B*4504 + B*5123		
B*4501 + B*570301	B*4504 + B*5707		
B*4501 + B*5802	B*4504 + B*5807		
B*4504 + B*51G1	B*5001 + B*5108		
B*4801 + B*51G1	B*4806 + B*520102		
B*4801 + B*510102	B*4806 + B*520101		
B*4801 + B*511301	B*4807 + B*510104		
B*4801 + B*511302	B*4807 + B*51G1		
B*4801 + B*780201	B*4806 + B*7805		
B*4806 + B*5606	B*780202 + B*8101		
B*4901 + B*780201	B*5001 + B*510102		
B*4901 + B*780202	B*5001 + B*51G1		
B*4901 + B*7805	B*5001 + B*520101		
B*4902 + B*5601	B*5001 + B*5607		
B*5001 + B*5123	B*5002 + B*510201		
B*5001 + B*5707	B*5002 + B*570301		
B*5001 + B*5807	B*5002 + B*5802		
B*51G1 + B*510202	B*510102 + B*510201		
B*51G1 + B*5110	B*5110 + B*5133		
B*51G1 + B*511301	B*510104 + B*511302		
B*51G1 + B*5131	B*5109 + B*5116		

B*51G1 + B*5134	B*510201 + B*5116		
B*51G1 + B*520101	B*510102 + B*520102		
B*51G1 + B*5301	B*5109 + B*5308	B*510201 + B*5302	
B*51G1 + B*5308	B*510202 + B*5306		
B*51G1 + B*5502	B*5121 + B*5601	B*5109 + B*5501	B*5606 + B*5901
B*51G1 + B*5601	B*5115 + B*5605		
B*51G1 + B*5602	B*5106 + B*5601		
B*51G1 + B*5609	B*5301 + B*5605		
B*51G1 + B*5610	B*5121 + B*5602	B*5106 + B*5502	
B*51G1 + B*5611	B*5304 + B*5605		
B*51G1 + B*5702	B*5129 + B*570301		
B*51G1 + B*5802	B*5109 + B*5806		
B*51G1 + B*780201	B*510102 + B*780202		
B*51G1 + B*7803	B*5122 + B*7801		
B*51G1 + B*7805	B*520101 + B*780202	B*520102 + B*780201	
B*510102 + B*5134	B*510202 + B*5116		
B*510102 + B*5301	B*510202 + B*5302		
B*510102 + B*7805	B*520101 + B*780201		
B*510201 + B*5131	B*5109 + B*5134		
B*510201 + B*520101	B*510202 + B*520102		
B*510201 + B*5707	B*5123 + B*570301		
B*510201 + B*5807	B*5123 + B*5802		
B*510201 + B*780201	B*510202 + B*780202		
B*5105 + B*5306	B*5129 + B*5301		
B*5105 + B*780202	B*5129 + B*7804		
B*5108 + B*7801	B*5120 + B*780202		
B*5115 + B*5609	B*5301 + B*5601		
B*5115 + B*5611	B*5304 + B*5601		
B*5116 + B*5301	B*5134 + B*5302	B*5131 + B*5308	
B*5116 + B*5502	B*5131 + B*5501		
B*5116 + B*5802	B*5131 + B*5806		
B*520102 + B*7804	B*5203 + B*780201		
B*5301 + B*5501	B*5308 + B*5502		
B*5301 + B*5502	B*5305 + B*5512		
B*5301 + B*5611	B*5304 + B*5609		
B*5301 + B*5806	B*5308 + B*5802		
B*5501 + B*5802	B*5502 + B*5806		
B*5502 + B*5602	B*5601 + B*5610		
B*570301 + B*5807	B*5707 + B*5802		

Alleles removed from analysis due to insertions or deletions

Allele

B*0808N

B*1307N

B*3925N

Alleles extended due to unsequenced regions

The following alleles contain unsequenced bases in exons 2 and or 3. For analysis these bases have been designated N, to indicate any possible base.

Allele

B*0803

B*1527

B*1530

B*1531

B*270503

B*3510

B*3907

B*3911

B*4405

B*4505

B*5110

B*670102

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